SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: ST. GEORGE-HYSLOP, PETER H
ROMMENS, JOHANNA M
FRASER, PAUL E

(ii) TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED TO ALZHEIMER'S DISEASE

(iii) NUMBER OF SEQUENCES: 183

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: LERNER, DAVID, LITTENBERG, KRUMHOLZ & MENTLIK
(B) STREET: 600 South Avenue West
(C) CITY: Westfield
(D) STATE: New Jersey
(E) COUNTRY: U.S.A.
(F) ZIP: 07090

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: Microsoft Word, Version 6.0c

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/509,359
(B) FILING DATE: 31-JUL-95
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Palisi, Thomas M.
(B) REGISTRATION NUMBER: 36629

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (908) 654-5000
(B) TELEFAX: (908) 654-7866

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2791 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TGGGACAGGC AGCTCCGGGG TCCGCGGTTT CACATCGGAA ACAAAACAGC GGCTGGTCTG 60

GAAGGAACCT GAGCTACGAG CCGCGGCGGC AGCGGGGCGG CGGGGNAAGC GTATACCTAA 120

TCTGGGAGCC TGCAAGTGAC AACAGCCTTT GCGGTCCTTA GACAGCTTGG CCTGGAGGAG 180

AACACATGAA AGAAAGAACC TCAAGAGGCT TTGTTTTCTG TGAAACAGTA TTTCTATACA 240

GTTGCTCCAA TGACAGAGTT ACCTGCACCG TTGTCCTACT TCCAGAATGC ACAGATGTCT 300

GAGGACAACC ACCTGAGCAA TACTGTACGT AGCCAGAATG ACAATAGAGA ACGGCAGGAG 360

CACAACGACA GACGGAGCCT TGGCCACCCT GAGCCATTAT CTAATGGACG ACCCCAGGGT 420

AACTCCCGGC AGGTGGTGGA GCAAGATGAG GAAGAAGATG AGGAGCTGAC ATTGAAATAT 480

GGCGCCAAGC ATGTGATCAT GCTCTTTGTC CCTGTGACTC TCTGCATGGT GGTGGTCGTG 540

GCTACCATTA AGTCAGTCAG CTTTTATACC CGGAAGGATG GGCAGCTAAT CTATACCCCA 600

TTCACAGAAG ATACCGAGAC TGTGGGCCAG AGAGCCCTGC ACTCAATTCT GAATGCTGCC 660

ATCATGATCA GTGTCATTGT TGTCATGACT ATCCTCCTGG TGGTTCTGTA TAAATACAGG 720

TGCTATAAGG TCATCCATGC CTGGCTTATT ATATCATCTC TATTGTTGCT GTTCTTTTTT 780

TCATTCATTT ACTTGGGGGA AGTGTTTAAA ACCTATAACG TTGCTGTGGA CTACATTACT 840

GTTGCACTCC TGATCTGGAA TTTGGGTGTG GTGGGAATGA TTTCCATTCA CTGGAAAGGT 900

CCACTTCGAC TCCAGCAGGC ATATCTCATT ATGATTAGTG CCCTCATGGC CCTGGTGTTT 960

ATCAAGTACC TCCCTGAATG GACTGCGTGG CTCATCTTGG CTGTGATTTC AGTATATGAT 1020

TTAGTGGCTG TTTTGTGTCC GAAAGGTCCA CTTCGTATGC TGGTTGAAAC AGCTCAGGAG 1080

AGAAATGAAA CGCTTTTTCC AGCTCTCATT TACTCCTCAA CAATGGTGTG GTTGGTGAAT 1140

ATGGCAGAAG GAGACCCGGA AGCTCAAAGG AGAGTATCCA AAAATTCCAA GTATAATGCA 1200

GAAAGCACAG AAAGGGAGTC ACAAGACACT GTTGCAGAGA ATGATGATGG CGGGTTCAGT 1260

GAGGAATGGG AAGCCCAGAG GGACAGTCAT CTAGGGCCTC ATCGCTCTAC ACCTGAGTCA 1320

CGAGCTGCTG TCCAGGAACT TTCCAGCAGT ATCCTCGCTG GTGAAGACCC AGAGGAAAGG 1380

GGAGTAAAAC TTGGATTGGG AGATTTCATT TTCTACAGTG TTCTGGTTGG TAAAGCCTCA 1440

GCAACAGCCA GTGGAGACTG GAACACAACC ATAGCCTGTT TCGTAGCCAT ATTAATTGGT 1500

TTGTGCCTTA CATTATTACT CCTTGCCATT TTCAAGAAAG CATTGCCAGC TCTTCCAATC 1560

TCCATCACCT TTGGGCTTGT TTTCTACTTT GCCACAGATT ATCTTGTACA GCCTTTTATG 1620

GACCAATTAG CATTCCATCA ATTTTATATC TAGCATATTT GCGGTTAGAA TCCCATGGAT 1680

GTTTCTTCTT TGACTATAAC CAAATCTGGG GAGGACAAAG GTGATTTTCC TGTGTCCACA 1740

TCTAACAAAG TCAAGATTCC CGGCTGGACT TTTGCAGCTT CCTTCCAAGT CTTCCTGACC 1800

ACCTTGCACT ATTGGACTTT GGAAGGAGGT GCCTATAGAA AACGATTTTG AACATACTTC 1860

ATCGCAGTGG ACTGTGTCCT CGGTGCAGAA ACTACCAGAT TTGAGGGACG AGGTCAAGGA 1920

GATATGATAG GCCCGGAAGT TGCTGTGCCC CATCAGCAGC TTGACGCGTG GTCACAGGAC 1980

GATTTCACTG ACACTGCGAA CTCTCAGGAC TACCGGTTAC CAAGAGGTTA GGTGAAGTGG 2040

TTTAAACCAA ACGGAACTCT TCATCTTAAA CTACACGTTG AAAATCAACC CAATAATTCT 2100

GTATTAACTG AATTCTGAAC TTTTCAGGAG GTACTGTGAG GAAGAGCAGG CACCAGCAGC 2160

AGAATGGGGA ATGGAGAGGT GGGCAGGGGT TCCAGCTTCC CTTTGATTTT TTGCTGCAGA 2220

CTCATCCTTT TTAAATGAGA CTTGTTTTCC CCTCTCTTTG AGTCAAGTCA AATATGTAGA 2280

TGCCTTTGGC AATTCTTCTT CTCAAGCACT GACACTCATT ACCGTCTGTG ATTGCCATTT 2340

CTTCCCAAGG CCAGTCTGAA CCTGAGGTTG CTTTATCCTA AAAGTTTTAA CCTCAGGTTC 2400

CAAATTCAGT AAATTTTGGA AACAGTACAG CTATTTCTCA TCAATTCTCT ATCATGTTGA 2460

AGTCAAATTT GGATTTTCCA CCAAATTCTG AATTTGTAGA CATACTTGTA CGCTCACTTG 2520

CCCCAGATGC CTCCTCTGTC CTCATTCTTC TCTCCCACAC AAGCAGTCTT TTTCTACAGC 2580

CAGTAAGGCA GCTCTGTCGT GGTAGCAGAT GGTCCCACTT ATTCTAGGGT CTTACTCTTT 2640

GTATGATGAA AAGAATGTGT TATGAATCGG TGCTGTCAGC CCTGCTGTCA GACCTTCTTC 2700

CACAGCAAAT GAGATGTATG CCCAAAGCGG TAGAATTAAA GAAGAGTAAA ATGGCTGTTG 2760

AAGCAAAAAA AAAAAAAAAA AAAAAAAAAA A 2791

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 467 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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Met Thr Glu Leu Pro Ala Pro Leu Ser Tyr Phe Gln Asn Ala Gln Met
1               5                  10                  15

Ser Glu Asp Asn His Leu Ser Asn Thr Val Arg Ser Gln Asn Asp Asn
            20                  25                  30

Arg Glu Arg Gln Glu His Asn Asp Arg Arg Ser Leu Gly His Pro Glu
        35                  40                  45
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Pro Leu Ser Asn Gly Arg Pro Gln Gly Asn Ser Arg Gln Val Val Glu
    50                  55                  60

Gln Asp Glu Glu Glu Asp Glu Glu Leu Thr Leu Lys Tyr Gly Ala Lys
65                  70                  75                  80

His Val Ile Met Leu Phe Val Pro Val Thr Leu Cys Met Val Val Val
                85                  90                  95

Val Ala Thr Ile Lys Ser Val Ser Phe Tyr Thr Arg Lys Asp Gly Gln
            100                 105                 110

Leu Ile Tyr Thr Pro Phe Thr Glu Asp Thr Glu Thr Val Gly Gln Arg
        115                 120                 125

Ala Leu His Ser Ile Leu Asn Ala Ala Ile Met Ile Ser Val Ile Val
    130                 135                 140

Val Met Thr Ile Leu Leu Val Val Leu Tyr Lys Tyr Arg Cys Tyr Lys
145                 150                 155                 160

Val Ile His Ala Trp Leu Ile Ile Ser Ser Leu Leu Leu Leu Phe Phe
                165                 170                 175

Phe Ser Phe Ile Tyr Leu Gly Glu Val Phe Lys Thr Tyr Asn Val Ala
            180                 185                 190

Val Asp Tyr Ile Thr Val Ala Leu Leu Ile Trp Asn Leu Gly Val Val
        195                 200                 205

Gly Met Ile Ser Ile His Trp Lys Gly Pro Leu Arg Leu Gln Gln Ala
    210                 215                 220

Tyr Leu Ile Met Ile Ser Ala Leu Met Ala Leu Val Phe Ile Lys Tyr
225                 230                 235                 240

Leu Pro Glu Trp Thr Ala Trp Leu Ile Leu Ala Val Ile Ser Val Tyr
                245                 250                 255

Asp Leu Val Ala Val Leu Cys Pro Lys Gly Pro Leu Arg Met Leu Val
            260                 265                 270

Glu Thr Ala Gln Glu Arg Asn Glu Thr Leu Phe Pro Ala Leu Ile Tyr
        275                 280                 285

Ser Ser Thr Met Val Trp Leu Val Asn Met Ala Glu Gly Asp Pro Glu
    290                 295                 300

Ala Gln Arg Arg Val Ser Lys Asn Ser Lys Tyr Asn Ala Glu Ser Thr
305                 310                 315                 320

Glu Arg Glu Ser Gln Asp Thr Val Ala Glu Asn Asp Asp Gly Gly Phe
                325                 330                 335

Ser Glu Glu Trp Glu Ala Gln Arg Asp Ser His Leu Gly Pro His Arg
            340                 345                 350
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Ser Thr Pro Glu Ser Arg Ala Ala Val Gln Glu Leu Ser Ser Ser Ile
355 360 365

Leu Ala Gly Glu Asp Pro Glu Glu Arg Gly Val Lys Leu Gly Leu Gly
370 375 380

Asp Phe Ile Phe Tyr Ser Val Leu Val Gly Lys Ala Ser Ala Thr Ala
385 390 395 400

Ser Gly Asp Trp Asn Thr Thr Ile Ala Cys Phe Val Ala Ile Leu Ile
405 410 415

Gly Leu Cys Leu Thr Leu Leu Leu Leu Ala Ile Phe Lys Lys Ala Leu
420 425 430

Pro Ala Leu Pro Ile Ser Ile Thr Phe Gly Leu Val Phe Tyr Phe Ala
435 440 445

Thr Asp Tyr Leu Val Gln Pro Phe Met Asp Gln Leu Ala Phe His Gln
450 455 460

Phe Tyr Ile
465

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1929 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ACCANACANC GGCAGCTGAG GCGGAAACCT AGGCTGCGAG CCGGCCGCCC GGGCGCGGAG 60

AGAGAAGGAA CCAACACAAG ACAGCAGCCC TTCGAGGTCT TTAGGCAGCT TGGAGGAGAA 120

CACATGAGAG AAAGAATCCC AAGAGGTTTT GTTTTCTTTG AGAAGGTATT TCTGTCCAGC 180

TGCTCCAATG ACAGAGATAC CTGCACCTTT GTCCTACTTC CAGAATGCCC AGATGTCTGA 240

GGACAGCCAC TCCAGCAGCG CCATCCGGAG CCAGAATGAC AGCCAAGAAC GGCAGCAGCA 300

GCATGACAGG CAGAGACTTG ACAACCCTGA GCCAATATCT AATGGGCGGC CCCAGAGTAA 360

CTCAAGACAG GTGGTGGAAC AAGATGAGGA GGAAGACGAA GAGCTGACAT TGAAATATGG 420

AGCCAAGCAT GTCATCATGC TCTTTGTCCC CGTGACCCTC TGCATGGTCG TCGTCGTGGC 480

CACCATCAAA TCAGTCAGCT TCTATACCCG GAAGGACGGT CAGCTAATCT ACACCCCATT 540

CACAGAAGAC ACTGAGACTG TAGGCCAAAG AGCCCTGCAC TCGATCCTGA ATGCGGCCAT 600

CATGATCAGT GTCATTGTCA TTATGACCAT CCTCCTGGTG GTCCTGTATA AATACAGGTG 660

CTACAAGGTC ATCCACGCCT GGCTTATTAT TTCATCTCTG TTGTTGCTGT TCTTTTTTTC 720

GTTCATTTAC TTAGGGGAAG TATTTAAGAC CTACAATGTC KCCGTGGACT ACGTTACAGT 780

AGCACTCCTA ATCTGGAATT GGGGTGTGGT CGGGATGATT GCCATCCACT GGAAAGGCCC 840

CCTTCGACTG CAGCAGGCGT ATCTCATTAT GATCAGTGCC CTCATGGCCC TGGTATTTAT 900

CAAGTACCTC CCCGAATGGA CCGCATGGCT CATCTTGGCT GTGATTTCAG TATATGATTT 960

GGTGGCTGTT TTATGTCCCA AAGGCCCACT TCGTATGCTG GTTGAAACAG CTCAGGAAAG 1020

AAATGAGACT CTCTTTCCAG CTCTTATCTA TTCCTCAACA ATGGTGTGGT TGGTGAATAT 1080

GGCTGAAGGA GACCCAGAAG CCCAAAGGAG GGTACCCAAG AACCCCAAGT ATAACACACA 1140

AAGAGCGGAG AGAGAGACAC AGGACAGTGG TTCTGGGAAC GATGATGGTG GCTTCAGTGA 1200

GGAGTGGGAG GCCCAAAGAG ACAGTCACCT GGGGCCTCAT CGCTCCACTC CCGAGTCAAG 1260

AGCTGCTGTC CAGGAACTTT CTGGGAGCAT TCTAACGAGT GAAGACCCGG AGGAAAGAGG 1320

AGTAAAACTT GGACTGGGAG ATTTCATTTT CTACAGTGTT CTGGTTGGTA AGGCCTCAGC 1380

AACCGCCAGT GGAGACTGGA ACACAACCAT AGCCTGCTTK GTAGCCATAC TGATCGGCCT 1440

GTGCCTTANA TTACTCCTGC TCGCCATTTA CAAGAAAGGG TNGCCAGCCC NCCCCATCTC 1500

CATCACCTTC GGGTTCGTGT TCTNCTTCGC CACGGATTAC CTTGTGCAGC CCTTCATGGA 1560

CCAACTTGCA TTCCATCAGT TTTATATCTA GCCTTTCTGC AGTTAGAACA TGGATGTTTC 1620

TTCTTTGATT ATCAAAAACA CAAAAACAGA GAGCAAGCCC GAGGAGGAGA CTGGTGACTT 1680

TCCTGTGTCC TCAGCTAACA AAGGCAGGAC TCCAGCTGGA CTTCTGCAGC TTCCTTCCGA 1740

GTCTCCCTAG CCACCCGCAC TACTGGACTG TGGAAGGAAG CGTCTACAGA GGAACGGTTT 1800

CCAACATCCA TCGCTGCAGC AGACGGTGTC CCTCAGTGAC TTGAGAGACA AGGACAAGGA 1860

AATGTGCTGG GCCAAGGAGC TGCCGTGCTC TGCTAGCTTT GGMCCGTGGG CATGGAGATT 1920

TACCCGCAC 1929

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 467 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```
Met Thr Glu Ile Pro Ala Pro Leu Ser Tyr Phe Gln Asn Ala Gln Met
1               5                  10                  15

Ser Glu Asp Ser His Ser Ser Ser Ala Ile Arg Ser Gln Asn Asp Ser
            20                  25                  30

Gln Glu Arg Gln Gln Gln His Asp Arg Gln Arg Leu Asp Asn Pro Glu
        35                  40                  45

Pro Ile Ser Asn Gly Arg Pro Gln Ser Asn Ser Arg Gln Val Val Glu
    50                  55                  60

Gln Asp Glu Glu Glu Asp Glu Glu Leu Thr Leu Lys Tyr Gly Ala Lys
65                  70                  75                  80

His Val Ile Met Leu Phe Val Pro Val Thr Leu Cys Met Val Val Val
                85                  90                  95

Val Ala Thr Ile Lys Ser Val Ser Phe Tyr Thr Arg Lys Asp Gly Gln
            100                 105                 110

Leu Ile Tyr Thr Pro Phe Thr Glu Asp Thr Glu Thr Val Gly Gln Arg
        115                 120                 125

Ala Leu His Ser Ile Leu Asn Ala Ala Ile Met Ile Ser Val Ile Val
    130                 135                 140

Ile Met Thr Ile Leu Leu Val Val Leu Tyr Lys Tyr Arg Cys Tyr Lys
145                 150                 155                 160

Val Ile His Ala Trp Leu Ile Ile Ser Ser Leu Leu Leu Leu Phe Phe
                165                 170                 175

Phe Ser Phe Ile Tyr Leu Gly Glu Val Phe Lys Thr Tyr Asn Val Xaa
            180                 185                 190

Val Asp Tyr Val Thr Val Ala Leu Leu Ile Trp Asn Trp Gly Val Val
        195                 200                 205

Gly Met Ile Ala Ile His Trp Lys Gly Pro Leu Arg Leu Gln Gln Ala
    210                 215                 220

Tyr Leu Ile Met Ile Ser Ala Leu Met Ala Leu Val Phe Ile Lys Tyr
225                 230                 235                 240

Leu Pro Glu Trp Thr Ala Trp Leu Ile Leu Ala Val Ile Ser Val Tyr
                245                 250                 255

Asp Leu Val Ala Val Leu Cys Pro Lys Gly Pro Leu Arg Met Leu Val
```

260 265 270

Glu Thr Ala Gln Glu Arg Asn Glu Thr Leu Phe Pro Ala Leu Ile Tyr
275 280 285

Ser Ser Thr Met Val Trp Leu Val Asn Met Ala Glu Gly Asp Pro Glu
290 295 300

Ala Gln Arg Arg Val Pro Lys Asn Pro Lys Tyr Asn Thr Gln Arg Ala
305 310 315 320

Glu Arg Glu Thr Gln Asp Ser Gly Ser Gly Asn Asp Asp Gly Gly Phe
325 330 335

Ser Glu Glu Trp Glu Ala Gln Arg Asp Ser His Leu Gly Pro His Arg
340 345 350

Ser Thr Pro Glu Ser Arg Ala Ala Val Gln Glu Leu Ser Gly Ser Ile
355 360 365

Leu Thr Ser Glu Asp Pro Glu Glu Arg Gly Val Lys Leu Gly Leu Gly
370 375 380

Asp Phe Ile Phe Tyr Ser Val Leu Val Gly Lys Ala Ser Ala Thr Ala
385 390 395 400

Ser Gly Asp Trp Asn Thr Thr Ile Ala Cys Xaa Val Ala Ile Leu Ile
405 410 415

Gly Leu Cys Leu Xaa Leu Leu Leu Leu Ala Ile Tyr Lys Lys Gly Xaa
420 425 430

Pro Ala Xaa Pro Ile Ser Ile Thr Phe Gly Phe Val Phe Xaa Phe Ala
435 440 445

Thr Asp Tyr Leu Val Gln Pro Phe Met Asp Gln Leu Ala Phe His Gln
450 455 460

Phe Tyr Ile
465

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3087 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GAATTCGGCA CGAGGGAAAT GCTGTTTGCT CGAAGACGTC TCAGGGCGCA GGTGCCTTGG 60

GCCGGGATTA GTAGCCGTCT GAACTGGAGT GGAGTAGGAG AAAGAGGAAG CGTCTTGGGC 120

TGGGTCTGCT TGAGCAACTG GTGAAACTCC GCGCCTCACG CCCCGGGTGT GTCCTTGTCC 180

AGGGGCGACG AGCATTCTGG GCGAAGTCCG CACSCCTCTT GTTCGAGGCG GAAGACGGGG 240

TCTGATSCTT TCTCCTTGGT CGGGMCTGTC TCGAGGCATG CATGTCCAGT GACTCTTGTG 300

TTTGCTGCTG CTTCCCTCTC AGATTCTTCT CACCGTTGTG GTCAGCTCTG CTTTAGGCAN 360

TATTAATCCA TAGTGGAGGC TGGGATGGGT GAGAGAATTG AGGTGACTTT TCCATAATTC 420

AGACCTAATC TGGGAGCCTG CAAGTGACAA CAGCCTTTGC GGTCCTTAGA CAGCTTGGCC 480

TGGAGGAGAA CACATGAAAG AAAGAACCTC AAGAGGCTTT GTTTTCTGTG AAACAGTATT 540

TCTATACAGT TGCTCCAATG ACAGAGTTAC CTGCACCGTT GTCCTACTTC CAGAATGCAC 600

AGATGTCTGA GGACAACCAC CTGAGCAATA CTAATGACAA TAGAGAACGG CAGGAGCACA 660

ACGACAGACG GAGCCTTGGC CACCCTGAGC CATTATCTAA TGGACGACCC CAGGGTAACT 720

CCCGGCAGGT GGTGGAGCAA GATGAGGAAG AAGATGAGGA GCTGACATTG AAATATGGCG 780

CCAAGCATGT GATCATGCTC TTTGTCCCTG TGACTCTCTG CATGGTGGTG GTCGTGGCTA 840

CCATTAAGTC AGTCAGCTTT TATACCCGGA AGGATGGGCA GCTAATCTAT ACCCCATTCA 900

CAGAAGATAC CGAGACTGTG GGCCAGAGAG CCCTGCACTC AATTCTGAAT GCTGCCATCA 960

TGATCAGTGT CATTGTTGTC ATGACTATCC TCCTGGTGGT TCTGTATAAA TACAGGTGCT 1020

ATAAGGTCAT CCATGCCTGG CTTATTATAT CATCTCTATT GTTGCTGTTC TTTTTTTCAT 1080

TCATTTACTT GGGGGAAGTG TTTAAAACCT ATAACGTTGC TGTGGACTAC ATTACTGTTG 1140

CACTCCTGAT CTGGAATTTG GGTGTGGTGG GAATGATTTC CATTCACTGG AAAGGTCCAC 1200

TTCGACTCCA GCAGGCATAT CTCATTATGA TTAGTGCCCT CATGGCCCTG GTGTTTATCA 1260

AGTACCTCCC TGAATGGACT GCGTGGCTCA TCTTGGCTGT GATTTCAGTA TATGATTTAG 1320

TGGCTGTTTT GTGTCCGAAA GGTCCACTTC GTATGCTGGT TGAAACAGCT CAGGAGAGAA 1380

ATGAAACGCT TTTTCCAGCT CTCATTTACT CCTCAACAAT GGTGTGGTTG GTGAATATGG 1440

CAGAAGGAGA CCCGGAAGCT CAAAGGAGAG TATCCAAAAA TTCCAAGTAT AATGCAGAAA 1500

GCACAGAAAG GGAGTCACAA GACACTGTTG CAGAGAATGA TGATGGCGGG TTCAGTGAGG 1560

AATGGGAAGC CCAGAGGGAC AGTCATCTAG GGCCTCATCG CTCTACACCT GAGTCACGAG 1620

CTGCTGTCCA GGAACTTTCC AGCAGTATCC TCGCTGGTGA AGACCCAGAG GAAAGGGGAG 1680

TAAAACTTGG ATTGGGAGAT TTCATTTTCT ACAGTGTTCT GGTTGGTAAA GCCTCAGCAA 1740

CAGCCAGTGG AGACTGGAAC ACAACCATAG CCTGTTTCGT AGCCATATTA ATTGGTTTGT 1800

GCCTTACATT ATTACTCCTT GCCATTTTCA AGAAAGCATT GCCAGCTCTT CCAATCTCCA 1860

TCACCTTTGG GCTTGTTTTC TACTTTGCCA CAGATTATCT TGTACAGCCT TTTATGGACC 1920

AATTAGCATT CCATCAATTT TATATCTAGC ATATTTGCGG TTAGAATCCC ATGGATGTTT 1980

CTTCTTTGAC TATAACCAAA TCTGGGGAGG ACAAAGGTGA TTTTCCTGTG TCCACATCTA 2040

ACAAAGTCAA GATTCCCGGC TGGACTTTTG CAGCTTCCTT CCAAGTCTTC CTGACCACCT 2100

TGCACTATTG GACTTTGGAA GGAGGTGCCT ATAGAAAACG ATTTTGAACA TACTTCATCG 2160

CAGTGGACTG TGTCCTCGGT GCAGAAACTA CCAGATTTGA GGGACGAGGT CAAGGAGATA 2220

TGATAGGCCC GGAAGTTGCT GTGCCCCATC AGCAGCTTGA CGCGTGGTCA CAGGACGATT 2280

TCACTGACAC TGCGAACTCT CAGGACTACC GGTTACCAAG AGGTTAGGTG AAGTGGTTTA 2340

AACCAAACGG AACTCTTCAT CTTAAACTAC ACGTTGAAAA TCAACCCAAT AATTCTGTAT 2400

TAACTGAATT CTGAACTTTT CAGGAGGTAC TGTGAGGAAG AGCAGGCACC AGCAGCAGAA 2460

TGGGGAATGG AGAGGTGGGC AGGGGTTCCA GCTTCCCTTT GATTTTTTGC TGCAGACTCA 2520

TCCTTTTTAA ATGAGACTTG TTTTCCCCTC TCTTTGAGTC AAGTCAAATA TGTAGATGCC 2580

TTTGGCAATT CTTCTTCTCA AGCACTGACA CTCATTACCG TCTGTGATTG CCATTTCTTC 2640

CCAAGGCCAG TCTGAACCTG AGGTTGCTTT ATCCTAAAAG TTTTAACCTC AGGTTCCAAA 2700

TTCAGTAAAT TTTGGAAACA GTACAGCTAT TTCTCATCAA TTCTCTATCA TGTTGAAGTC 2760

AAATTTGGAT TTTCCACCAA ATTCTGAATT TGTAGACATA CTTGTACGCT CACTTGCCCC 2820

AGATGCCTCC TCTGTCCTCA TTCTTCTCTC CCACACAAGC AGTCTTTTTC TACAGCCAGT 2880

AAGGCAGCTC TGTCGTGGTA GCAGATGGTC CCACTTATTC TAGGGTCTTA CTCTTTGTAT 2940

GATGAAAAGA ATGTGTTATG AATCGGTGCT GTCAGCCCTG CTGTCAGACC TTCTTCCACA 3000

GCAAATGAGA TGTATGCCCA AAGCGGTAGA ATTAAAGAAG AGTAAAATGG CTGTTGAAGC 3060

AAAAAAAAAA AAAAAAAAAA AAAAAAA 3087

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 945 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GTTNTCCNAA CCAACTTAGG AGNTTGGACC TGGGRAAGAC CNACNTGATC TCCGGGAGGN 60

AAAGACTNCA GTTGAGCCGT GATTGCACCC ACTTTACTCC AAGCCTGGGC AACCAAAATG 120

AGACACTGGC TCCAAACACA AAAACAAAAA CAAAAAAAGA GTAAATTAAT TTANAGGGAA 180

GNATTAAATA AATAATAGCA CAGTTGATAT AGGTTATGGT AAAATTATAA AGGTGGGANA 240

TTAATATCTA ATGTTTGGGA GCCATCACAT TATTCTAAAT AATGTTTTGG TGGAAATTAT 300

TGTACATCTT TTAAAATCTG TGTAATTTTT TTTCAGGGAA GTGTTTAAAA CCTATAACGT 360

TGCTGTGGAC TACATTACTG TTNCACTCCT GATCTGGAAT TTTGGTGTGG TGGGAATGAT 420

TTCCATTCAC TGGAAAGGTC CACTTCGACT CCAGCAGGCA TATCTCATTA TGATTAGTGC 480

CCTCATGNCC CTGKTGTTTA TCAAGTACCT CCCTGAATGG ACTGNGTGGC TCATCTTGGC 540

TGTGATTTCA GTATATGGTA AAACCCAAGA CTGATAATTT GTTTGTCACA GGAATGCCCC 600

ACTGGAGTGT TTTCTTTCCT CATCTCTTTA TCTTGATTTA GAGAAAATGG TAACGTGTAC 660

ATCCCATAAC TCTTCAGTAA ATCATTAATT AGCTATAGTA ACTTTTTCAT TTGAAGATTT 720

CGGCTGGGCA TGGTAGCTCA TGCCTGTAAT CTTAGCACTT TGGGAGGCTG AGGCGGGCAG 780

ATCACCTAAG CCCAGAGTTC AAGACCAGCC TGGGCAACAT GGCAAAACCT CGTATCTACA 840

GAAAATACAA AAATTAGCCG GGCATGGTGG TGCACACCTG TAGTTCCAGC TACTTAGGAG 900

GCTGAGGTGG GAGGATCGAT TGATCCCAGG AGGTCAAGNC TGCAG 945

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 450 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GTTGCAAAGT CATGGATTCC TTTAGGTAGC TACATTATCA ACCTTTTTGA GAATAAAATG 60

AATTGAGAGT GTTACAGTCT AATTCTATAT CACATGTAAC TTTTATTTGG ATATATCAGT 120

AATAGTGCTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTGGGGANA GAGTCTCGCT 180

CTGTCGCCAG GTTGGAGTGC AATGGTGCGA TCTTGGCTCA CTGAAAGCTC CACCNCCCGG 240

GTTCAAGTGA TTCTCCTGCC TCAGCCNCCC AAGTAGNTGG GACTACAGGG GTGCGCCACC 300

ACGCCTGGGA TAATTTTGGG NTTTTTAGTA GAGATGGCGT TTCACCANCT TGGNGCAGGC 360

TGGTCTTGGA ACTCCTGANA TCATGATCTG CCTGCCTTAG CCTCCCCAAA GTGCTGGGAT 420

TNCAGGGGTG AGCCACTGTT CCTGGGCCTC 450

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 516 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GCTCATCATG CTTCACGGGG GAGGCTGTGC GGGAAGAATG CTCCCACACA GNATAAAGAA 60

TGCTCCCGCA CAGGATAGAG AATGCCCCCG CACAGCATAG AGAAGCCCCC GCACAGCATA 120

GAGAATGCCC CCNCACAGCA TAGAGAAGCC CCCGCACAGC ATAGAGAATG CTCTTCACCT 180

CTGGGTTTTT AACCAGCCAA ACTAAAATCA CAGAGGSCMA CACATCATTT AAGATAGAAA 240

TTTCTGTATC TTTTAATTTY TTTCMAAGTA GTTTTACTTA TTTTCAGATT CTATTTCTTT 300

ACTAGAATTA AGGGATAAAA TAACAATGTG TGCATAATGA ACCCTATGAA ACMAACMMAA 360

GCTAGGTTTT TTTCATAGST CTTCTTCCAG ATTGAATGAA CGTCTGTTCT AAAATTTAAC 420

CCCCCAGGGA AATATTCAGT TAACTATGTT AAAAACCCAG ACTTGTGATT GAGTTTTGCC 480

TGAAAATGCT TTCATAATTA TGTGTGAATG TGTGTC 516

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1726 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGATCCCTCC CCTTTTTAGA CCATACAAGG TAACTTCCGG ACGTTGCCAT GGCATCTGTA 60

AACTGTCATG GTGTTGGCGG GGAGTGTCTT TTAGCATGCT AATGTATTAT AATTAGCGTA 120

TAGTGAGCAG TGAGGATAAC CAGAGGTCAC TCTCCTCACC ATCTTGGTTT TGGTGGGTTT 180

TGGCCAGCTT CTTTATTGCA ACCAGTTTTA TCAGCAAGAT CTTTATGAGC TGTATCTTGT 240

GCTGACTTCC TATCTCATCC CGNAACTAAG AGTACCTAAC CTCCTGCAAA TTGMAGNCCA 300

GNAGGTCTTG GNCTTATTTN ACCCAGCCCC TATTCAARAT AGAGTNGYTC TTGGNCCAAA 360

CGCCYCTGAC ACAAGGATTT TAAAGTCTTA TTAATTAAGG TAAGATAGKT CCTTGSATAT 420

GTGGTCTGAA ATCACAGAAA GCTGAATTTG GAAAAAGGTG CTTGGASCTG CAGCCAGTAA 480

ACAAGTTTTC ATGCAGGTGT CAGTATTTAA GGTACATCTC AAAGGATAAG TACAATTGTG 540

TATGTTGGGA TGAACAGAGA GAATGGAGCA ANCCAAGACC CAGGTAAAAG AGAGGACCTG 600

AATGCCTTCA GTGAACAATG ATAGATAATC TAGACTTTTA AACTGCATAC TTCCTGTACA 660

TTGTTTTTTC TTGCTTCAGG TTTTTAGAAC TCATAGTGAC GGGTCTGTTG TTAATCCCAG 720

GTCTAACCGT TACCTTGATT CTGCTGAGAA TCTGATTTAC TGAAAATGTT TTTCTTGTGC 780

TTATAGAATG ACAATAGAGA ACGGCAGGAG CACAACGACA GACGGAGCCT TGGCCACCCT 840

GANCCATTAT CTAATGGACG ACCCAGGGTA ACTCCCGGCA GGTGGTGGAN CAAGATGAGG 900

AAGAAGATGA GGANCTGACA TTGAAATATG NCGSCAAGCA TGTGATCATG CTCTTTGKCC 960

CTGTGACTCT CTGCATGGTG GTGGTCGTGG NTACCATTAA GTCAGTCAGC TTTTATACCC 1020

GGAAGGATGG GCAGCTGTAC GTATGAGTTT KGTTTTATTA TTCTCAAASC CAGTGTGGCT 1080

TTTCTTTACA GCATGTCATC ATCACCTTGA AGGCCTCTNC ATTGAAGGGG CATGACTTAG 1140

CTGGAGAGCC CATCCTCTGT GATGGTCAGG AGCAGTTGAG AGANCGAGGG GTTATTACTT 1200

CATGTTTTAA GTGGAGAAAA GGAACACTGC AGAAGTATGT TTCCTGTATG GTATTACTGG 1260

ATAGGGCTGA AGTTATGCTG AATTGAACAC ATAAATTCTT TTCCACCTCA GGGNCATTGG 1320

GCGCCCATTG NTCTTCTGCC TAGAATATTC TTTCCTTTNC TNACTTKGGN GGATTAAATT 1380

CCTGTCATCC CCCTCCTCTT GGTGTTATAT ATAAAGTNTT GGTGCCGCAA AAGAAGTAGC 1440

ACTCGAATAT AAAATTTTCC TTTTAATTCT CAGCAAGGNA AGTTACTTCT ATATAGAAGG 1500

GTGCACCCNT ACAGATGGAA CAATGGCAAG CGCACATTTG GGACAAGGGA GGGGAAAGGG 1560

TTCTTATCCC TGACACACGT GGTCCCNGCT GNTGTGTNCT NCCCCCACTG ANTAGGGTTA 1620

GACTGGACAG GCTTAAACTA ATTCCAATTG GNTAATTTAA AGAGAATNAT GGGGTGAATG 1680

CTTTGGGAGG AGTCAAGGAA GAGNAGGTAG NAGGTAACTT GAATGA 1726

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1883 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CNCGTATAAA AGACCAACAT TGCCANCNAC AACCACAGGC AAGATCTTCT CCTACCTTCC 60

CCCNNGGTGT AATACCAAGT ATTCNCCAAT TTGTGATAAA CTTTCATTGG AAAGTGACCA 120

CCCTCCTTGG TTAATACATT GTCTGTGCCT GCTTTCACAC TACAGTAGCA CAGTTGAGTG 180

TTTGCCCTGG AGACCATATG ACCCATAGAG CTTAAAATAT TCAGTCTGGC TTTTTACAGA 240

GATGTTTCTG ACTTTGTTAA TAGAAAATCA ACCCAACTGG TTTAAATAAT GCACATACTT 300

TCTCTCTCAT AGAGTAGTGC AGAGGTAGNC AGTCCAGATT AGTASGGTGG CTTCACGTTC 360

ATCCAAGGAC TCAATCTCCT TCTTTCTTCT TTAGCTTCTA ACCTCTAGCT TACTTCAGGG 420

TCCAGGCTGG AGCCCTASCC TTCATTTCTG ACAGTAGGAA GGAGTAGGGG AGAAAAGAAC 480

ATAGGACATG TCAGCAGAAT TCTCTCCTTA GAAGTTCCAT ACACAACACA TCTCCCTAGA 540

AGTCATTGCC CTTACTTGTT CTCATAGCCA TCCTAAATAT AAGGGAGTCA GAAGTAAAGT 600

CTKKNTGGCT GGGAATATTG GCACCTGGAA TAAAAATGTT TTTCTGTGAA TGAGAAACAA 660

GGGGAAGATG GATATGTGAC ATTATCTTAA GACAACTCCA GTTGCAATTA CTCTGCAGAT 720

GAGAGGCACT AATTATAAGC CATATTACCT TTCTTCTGAC AACCACTTGT CAGCCCNCGT 780

GGTTTCTGTG GCAGAATCTG GTTCYATAMC AAGTTCCTAA TAANCTGTAS CCNAAAAAAT 840

TTGATGAGGT ATTATAATTA TTTCAATATA AAGCACCCAC TAGATGGAGC CAGTGTCTGC 900

TTCACATGTT AAGTCCTTCT TTCCATATGT TAGACATTTT CTTTGAAGCA ATTTTAGAGT 960

GTAGCTGTTT TTCTCAGGTT AAAAATTCTT AGCTAGGATT GGTGAGTTGG GGAAAAGTGA 1020

CTTATAAGAT NCGAATTGAA TTAAGAAAAA GAAAATTCTG TGTTGGAGGT GGTAATGTGG 1080

KTGGTGATCT YCATTAACAC TGANCTAGGG CTTTKGKGTT TGKTTTATTG TAGAATCTAT 1140

ACCCCATTCA NAGAAGATAC CGAGACTGTG GGCCAGAGAG CCCTGCACTC AATTCTGAAT 1200

GCTGCCATCA TGATCAGNGT CATTGTWGTC ATGACTANNC TCCTGGTGGT TCWGTATAAA 1260

TACAGGTGCT ATAAGGTGAG CATGAGACAC AGATCTTTGN TTTCCACCCT GTTCTTCTTA 1320

TGGTTGGGTA TTCTTGTCAC AGTAACTTAA CTGATCTAGG AAAGAAAAAA TGTTTTGTCT 1380

TCTAGAGATA AGTTAATTTT TAGTTTTCTT CCTCCTCACT GTGGAACATT CAAAAAATAC 1440

AAAAAGGAAG CCAGGTGCAT GTGTAATGCC AGGCTCAGAG GCTGAGGCAG GAGGATCGCT 1500

TGGGCCCAGG AGTTCACAAG CAGCTTGGGC AACGTAGCAA GACCCTGCCT CTATTAAAGA 1560

AAACAAAAAA CAAATATTGG AAGTATTTTA TATGCATGGA ATCTATATGT CATGAAAAAA 1620

TTAGTGTAAA ATATATATAT TATGATTAGN TATCAAGATT TAGTGATAAT TTATGTTATT 1680

TTGGGATTTC AATGCCTTTT TAGGCCATTG TCTCAAMAAA TAAAAGCAGA AAACAAAAAA 1740

AGTTGTAACT GAAAAATAAA CATTTCCATA TAATAGCACA ATCTAAGTGG GTTTTTGNTT 1800

GTTTGTTTGN TTGTTGAAGC AGGGCCTTGC CCTNYCACCC AGGNTGGAGT GAAGTGCAGT 1860

GGCACGATTT TGGCTCACTG CAG 1883

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 823 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CAGGAGTGGA CTAGGTAAAT GNAAGNTGTT TTAAAGAGAG ATGNGGNCNG GGACATAGTG 60

GTACACANCT GTAATGCTCA NCACTKATGG GGAGTACTGA AGGNGGNSGG ATCACTTGNG 120

GGTCNGGAAT NTGAGANCAG CCTGGGCAAN ATGGCGAAAC CCTGTCTCTA CTAAAAATAG 180

CCANAAWNWA GCCTAGCGTG GTGGCGCRCA CGCGTGGTTC CACCTACTCA GGAGGCNTAA 240

GCACGAGNAN TNCTTGAACC CAGGAGGCAG AGGNTGTGGT GARCTGAGAT CGTGCCACTG 300

CACTCCAGTC TGGGCGACMA AGTGAGACCC TGTCTCCNNN AAGAAAAAAA AAATCTGTAC 360

TTTTTAAGGG TTGTGGGACC TGTTAATTAT ATTGAAATGC TTCTYTTCTA GGTCATCCAT 420

GCCTGGCTTA TTATATCATC TCTATTGTTG CTGCTCTTTT TTACATTCAT TTACTTGGGG 480

TAAGTTGTGA AATTTGGGGT CTGTCTTTCA GAATTAACTA CCTNNGTGCT GTGTAGCTAT 540

CATTTAAAGC CATGTACTTT GNTGATGAAT TACTCTGAAG TTTTAATTGT NTCCACATAT 600

AGGTCATACT TGGTATATAA AAGACTAGNC AGTATTACTA ATTGAGACAT TCTTCTGTNG 660

CTCCTNGCTT ATAATAAGTA GAACTGAAAG NAACTTAAGA CTACAGTTAA TTCTAAGCCT 720

TTGGGGAAGG ATTATATAGC CTTCTAGTAG GAAGTCTTGT GCNATCAGAA TGTTTNTAAA 780

GAAAGGGTNT CAAGGAATNG TATAAANACC AAAAATAATT GAT 823

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 736 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GTCTTTCCCA TCTTCTCCAC AGAGTTTGTG CCTTACATTA TTACTCCTTG CCATTTTCAA 60

GAAAGCATTG TCAGCTCTTC CAATCTCCAT CACCTTTGGG CTTGTTTTCT ACTTTGCCAC 120

AGATTATCTT GTACAGCCTT TTATGGACCA ATTAGCATTC CATCAATTTT ATATCTAGCA 180

TATTTGCGGT TAGAATCCCA TGGATGTTTC TTCTTTGACT ATAACAAAAT CTGGGGAGGA 240

CAAAGGTGAT TTCCTGTGTC CACATCTAAC AAATCAAGAT CCCCGGCTGG ACTTTTGGAG 300

GTTCCTTCCA AGTCTTCCTG ACCACCTTGC ACTATTGGAC TTTGGAAGGA GGTGCCTATA 360

GAAAACGATT TTGAACATAC TTCATCGCAG TGGACTGTGT CCTCGGTGCA GAAACTACCA 420

GATTTGAGGG ACGAGGTCAA GGAGATATGA TAGGCCCGGA AGTTGCTGTG CCCCATCAGC 480

AGCTTGACGC GTGGTCACAG GACGATTTTC ACTGACACTG CGAACTCTCA GGACTACCGT 540

TACCAAGAGG TTAGGTGAAG TGGTTTAAAC CAAACGGAAC TCTTCATCTT AAACTACACG 600

TTGAAAATCA ACCCAATAAT TCTGTATTAA CTGAATTCTG AACTTTTCAG GAGGTACTGT 660

GAGGAAGAGC AGGCACCACC AGCAGAATGG GGAATGGAGA GGTGGGCAGG GGTTCCAGCT 720

TCCCTTTGAT TTTTTG 736

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 893 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GGATCCGCCC GCCTTGGCCT CCCAAAGTGC TGGGATTACA GGCATGAGCC ACCGCTCCTG 60

GCTGAGTCTG CGATTTCTTG CCAGCTCTAC CCAGTTGTGT CATCTTAAGC AAGTCACTGA 120

ACTTCTCTGG ATTCCCTTCT CCTNNWGTAA AATAAGNATG TTATCTGNCC NNCCTGCCTT 180

GGGCATTGTG ATAAGGATAA GATGACATTA TAGAATNTNG CAAAATTAAA AGCGCTAGAC 240

AAATGATTTT ATGAAAATAT AAAGATTAGN TTGAGTTTGG GCCAGCATAG AAAAAGGAAT 300

GTTGAGAACA TTCCNTTAAG GATTACTCAA GCYCCCCTTT TGSTGKNWAA TCAGANNGTC 360

ATNNAMNTAT CNTNTGTGGG YTGAAAATGT TTGGTTGTCT CAGGCGGTTC CTACTTATTG 420

CTAAAGAGTC CTACCTTGAG CTTATAGTAA ATTTGTCAGT TAGTTGAAAG TCGTGACAAA 480

TTAATACATT CCTGGTTTAC AAATTGGTCT TATAAGTATT TGATTGGTNT AAATGNATTT 540

ACTAGGATTT AACTAACAAT GGATGACCTG GTGAAATCCT ATTTCAGACC TAATCTGGGA 600

GCCTGCAAGT GACAACAGCC TTTGCGGTCC TTAGACAGCT TGGCCTGGAG GAGAACACAT 660

GAAAGAAAGG TTTGTTTCTG CTTAATGTAA TCTATGGAAG TGTTTTTTAT AACAGTATAA 720

TTGTAGTGCA CAAAGTTCTG TTTTTCTTTC CCTTTTCAGA ACCTCAAGAG GCTTTGTTTT 780

CTGTGAAACA GTATTTCTAT ACAGTNTGCT CCAANTGNAC AGAGTTACCT GCACNNCGTT 840

GTCCNTACTT CCAGAATGCA CAGATGTCTG AGGACAACCA CCTGAGCAAT ACT 893

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 475 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TCAGAAAATA CTTTNGGGCA CATGAGAATC ACATGAGAAC AAGCTGATGC ATAATTCCTC 60

CTGTGATGGA ATGTAATAGT AATTTAACAG TGTCCTTTCT TTTTAACTGC CTCAAGGATA 120

CAGCAAAATA AAACAAAAGC AATATGAAGG CTGAGAATAG GTATCAGATT ATCATAAAAA 180

GTATAGATCA AAAGGAATCT GGTKCTNAGG TTGGCGCAGC AGCCTCTAGA AGCGACNAGG 240

GAGACTTTTA GAACTACCAT TCTCCTCTAT AAGTGGATCC NANGCCCAGG RAAACTTGAT 300

ATTGAGNACA ATGGCCTTAC TGAAATAACC TGTGATCCAC TCGGNCTCAT CATCTCCACC 360

ACCACCATAA ATTTGATGAG TNCCTATAAT ATTCCANCCA GNGGAAATAC CTGGRAGGTT 420

ACTGAAAGGC NACNATCAGA CNAAAATAAA GNATACCGTA GGTAAATTCT ACAGT 475

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 180 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GTTCTCNAGA TCTCTTCAAA ATTCATTNTG CGCTATAGGA GCTGGGATTA CCGCGGGTGC 60

TGGAACCAGA CTTGCNCTCC AATGGATCCT CCANACNGGA NGGGGGGTGG ACTCACACCA 120

TTTACAGGGG GCTCGTAAAG AATCCTGTTT TGANTATTNT NCCGTCAATT ACCNCCCCAA 180

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 457 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

AATGTAACMA CMAAACCYCA AACTCCTGNA AGAANATGGT TACTTATNGA TNCCATTTNC 60

TTTTTNCACT CTCAGACATA AATATAAACM MANTTTCTAC TGTGGRAAAA CATCTNCAGG 120

GGNCNTTTAN CCATGATCTC TAGNACNANG GGCTNGTGGN TNGTTTTAAT GTCTCTAAGC 180

NACTNGACTA GTTTCTCTTN CACTGAGNAA ACTGCNACAA GTNNTTNCTN CTGNATCTGN 240

ACTGNAATGC TAAGTTNCAA GTNCCAATGA GCTNGTGANT TANYCTTTAT TTNAMCNAAA 300

GTNNTTAATC ANCCNCAGTG TTACTTTGNA AAGCTNCTCC CTGGACAGGC GGCCCNACTT 360

CTAATGTTAT GAATGGGCTG GAGNANCCTC NACNTGAGTT TNNWAAGGNT CAACANCCAA 420

TRGNAANTGT AMCCGACTCT AAATTCCAAC CNATAAT 457

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 373 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ATCTGTGCTA GGTAGTGTAC TAATCATTCA GTTTATCTCA TTTAATCTNN ATGNAACTCT 60

AAGTCATTCG CTNTGANCNA CACATAACAG ATCTCGCAAC TGNAGTTTAG CGAGGCCAGT 120

TAATTTKCCA AAGNTCATAA TNCTAAGNAG TTCTAGNATG GAGATTCMAA GTCCNACTGT 180

TTAGTCAAGA GACCCTACTG TTAACTAGTA CCTTTACACT ACTAACTGGG TAANCCATAA 240

NCAATTAATG ATAAAGATTG AGATTACTKC CACATTCTCA CTGGTTATAA ATTAAAACNT 300

CAAATAAAAA NTCTTGGCAC TTCTATGGTA ATATTTTTAT TAGGATAAAC TTTCAAGNAG 360

TGGATNCTAG GTG 373

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 422 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CCCACACTGN TGGGCCATGG AAGCCATGAG TGTACCACAT GGCCCTGTCC CACTGGCCAC 60

AGTNGATTGG TTGGNTCGGG AGTAGTCACC TGATTCAAGN TGGGCCAATC AGATCCTACC 120

TCCANGGGGT TNGGAATTAG AAAACAGTGA CCCTAGYTAG TNTAGGCNAC TTGAACTGGA 180

GGGCCCATAC ATTCAGGAGC CTTATGGGGC CATGTACACA TGGAAGCAGG AAGANTGAAG 240

GAGGGAGAAG TAGAGGCCAG AAACCCACCT GGGTTCCTGT TTCCCAATGN TAAGTCCCTG 300

CCATGTYCCT GCTCTTCCTG TGGTTNGGAT CTTCAAAGGT TGCTCAAATT NGGGGCAGTG 360

GCCCTGGCAG CTTTTCAAAT CCTYCCCATT TTTATTGAAG CTGAAAGACC CTTGACTAGA 420

AC 422

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 395 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

ATTGTTATTT TTCGTCACTA CCTCCCCGGG TCGGGAGTGG GTAATTTGCG CGCCTGCTGC 60

CTTCCTTGGA TGTGGTAGCC GTTTCTCAGG CTCCCTCTCC GGAATCGAAC CCTGATTCCC 120

CGTCACCCGT GGTCACCATG GTTAGGCACG GCGACTACCA TCGAAAGTTA ATAGGGCAGA 180

TCTCGAGAAT TCTCGAGATC TCCNTCMAAT TATTACTTCA NTTKCGGTAG TGATCAGNAC 240

NAGGCAGTTC TATTGATTTC TCTCCTTTCA TTCTGAGTTT CTCCATAAAT TAATTGGACC 300

TAATCATGTT TKNAATCCTG TCTTTTAGGG GGNANTTGNA CTNTCAAGTG TTTAAAGGGA 360

GGGNCGGAGN ATGATTNTGG ATTGGAGTGA GAGCA 395

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 487 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CAGANTTTCT GGGTNAAAAG GACCTNANAC ATAATATAGT GGACTTNCAA TAAACACTTA 60

CCAAATGGAN AAATGAACCC CTGGTCACCC CGATCTCACT AGTNCCTNCC CTGAAACCCG 120

ANANATCTGA GTCCTTTTCT CCTTTACTAA CCCTTNCTCC AATCCTGCTC ATGGGAATTA 180

ANGNTGTAAA ATANGCCTGG GGNACCTCGG RCCTCTNCCC TGGGNTCTGT GGGTGGGAGN 240

ACTGTGGAAG CCGTWTCAAT CGCCCCCACC TATGAGAGCC TTTCTNCAGG GCCAGCCATG 300

AACGTCCCCC ATGTNATCAG NATCTNCAGG CTACTGCTGT CCTTCYTGGA TWTTTAACCT 360

GGRGGCGGGC CAGGGACAGA AAARGGAGGT GGCAAGATCC TTGAACAAAA GGAGCTATAA 420

AAGGGCGTTG GGGGAAGCAA GGCAAACGGC AGATTAAACA AGCAGGCACC TCAAGGAAAC 480

GTGACGC 487

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 500 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CTCGAGATCT GGCCCATCAT TTAGTTTTAT NGCTTGNAGT NTNTAGNAGA TAAAACATCC 60

ACGTGGATCT NCTCTTAGAG AAATCAANTA CTTTAGGNAT NTGATAGTCA GAGANTGGNT 120

ATCAAATNGA AAGGNATNTN GGTNGANCAG TTAGTTNGYN CCNTTNGNNG AGACCACTGG 180

GNTGTNGASA CCAGATTCMK GGGTNCNAAT CTTANGGTAA TCTNAGAGCC AACACATGGG 240

TCATNTTATS CCCCAAACTT AGCCACATCT BGTGGGGYTA TGGNGTCACC CCAAGAGCAG 300

GAGGAGCATG GNTGGATGGA AATCCATCTC CACCACTGGA ACCCCAAWTT CTGAATGNAT 360

CACCTGTTAG AGTTTCTTGT YCATAAAATA GCAGGGAATT TAGGAATTTA GTTTTTTTTT 420

AATAGTTTGG GCCTTTTATC CACACTCTCA GGAGCTTAGG ATACTTTTCT CCTTCAGCTC 480

ACTCTGAAAC TCCCTCTGGA 500

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 406 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TCGAGATCTG TGGTAGTNAC ATGATATTCT GGCAMCTACT TTCATTATCA CCTTTATTAA 60

AATAAATTTA AAGAAAAATG GCAGTATGTT TCTGTGRAGN CCACGAGTAC TCATTTTAAA 120

GGACTCMAGA GTTNCAGRNA AGTAAAAAGR AAAGAGTAAA ATCATTTTCT AANTYTYWYY 180

TTCCAGAAAT AACGATGTTG AGCATTAAGT GGACTTCATT TCATACTCTT TCMMAGNTTA 240

TGTAGGCATA WAWATGTGTG TGTATATACA TATATATGGG TACATCCTTA GAGAAGTTGG 300

CTGGCTAGAT AGACACACNT NAAAAATGGR ATCATACTCT AATKCCATTT NNANTTTANA 360

AAATACATAT TCAGANCCNC TGTNCTTATA NACAGAGTAA NTGAAA 406

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 289 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GACCCAGTAA AACTTATCTC ATGAGCATAA GGCTGAATGG GATTGACAGC CTACAGAACC 60

CGGATTTTAT CATGAGGGCA TTAGTGGGGG TTGGGGGTTA GGTACTGAAA GTTTAAGGAG 120

GTGAAAGGAA AGCAACTTGT GCCTTACAGG GTCAAGCTAG GTCAAGGAAA TTCCCAGGAG 180

CGTGTGGAAG CTCTCTACCT GATAGGTGAG CTCAAGCTTA TGACCGCCCA AGCTTCTCCC 240

CAAGCTTCCC TTCCACTGCT TCCTCTTGAT TGACTTCCAC AGCAAGGTC 289

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 367 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CCATCAGGAT TTACTGAGTA AAAATCTCAG GTNTTAACCA TGCCCCTAAA ATGTGCTATN 60

CCAAAGAGGA ACAGGTTACT TGGGAGGAAA AAAGCTGCCT GGGNAACTCC CCNCAAATGT 120

TTATTTTAAA TAAAAATGGT NGATGGAAAT ATTTTNTAAA AGAACTTGGG GTNTAATATG 180

GNATACTGCC CATCAAACAA AAAAGGAAAT AAAACTTCNT TCCCATTTAT AATAAGTTNC 240

CCACCCTTTA CTATCAAGAT TACAACTTAT TGACCTTTTA TGCTNGCTNG GTTTTTTTGG 300

GACTGCCTAA TCCAATGTTT AAATTTTCTA NGTCTGNATT TCAATGTGGG TAGGAGTNAT 360

TTTTCAA 367

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 425 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GAGTATCTGA CAGGTAAGAT TGCTTTTTAA AGTTGTTTTA AATGCATTAC ATGACTGAGA 60

AAAGAAAAAT GCACATTTTA TTGTTGCAGT TTAAAATTTC ATTTNGNGTG AAACTAAACG 120

TGAAACAAAA GGGATAAATG TGTTTTGNTT TTGTTTTGGT TTTACCTGTT TGGGGTATTT 180

TTTTCTGAGT TTGTGTAGAA ACCCGTGTGG NTACACTGGG TAATCTTGTC AGGGNTACMA 240

AMCTTGGGTC TTGANTTTGG TTANTTGGNT TTANTTGGTG NACCCATGTA CTTGCTCTTC 300

CNTCCCAGAA ACATAGCTTG GTAGGCNAGG GTTAANCCAG TGTCGGCGAN CCCATGTCCC 360

TANCACAGCA TCTTGTAAGT TTAATGCACA ATCGTTCCNT CCCAGGATGG ANTTATCATT 420

ATAAA 425

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2377 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GAGAGGCGCA GGAGCCACAA ATAAAGCAAG AGCCAGAATC AGAAGNGGAG GAAGAAGAAA 60

AGCAAGAAAA AGRAGRAANA CGAGAAGAAC CCATGGRAGA GGAAGAGGAN CCAGANCMAA 120

AGCCTTGTCT GAAACCTACT CTGAGGCCCA TCAGCTCTGC TCCATCTGTT TCCTCTGCCA 180

GTGGNAATGC NACACCTAAC ACTCCTGGGG ATGAGTCTCC CTGTGGTATT ATTATTCCTC 240

ATGRAAACTC ACCAGATCAA CAGCAACCTG AGGAGCATAG GCCMAAAATA GGACTAAGTC 300

TTAAACTGGG TGCTTCCAAT AGTCCTGGTC AGCCTAATTC TGTGAAGAGA AAGAAACTAC 360

CTGTAGATAG TGTCTTTAAC AAATTTGAGG ATGAAGACAG TGATGACGTA CCCCGAAAAA 420

GGAAACTGGT TCCCTTGGAT TATGGTGAAG ATGATAAAAA TNCAACCAAA GGCACTGTAA 480

ACACTGAAGA AAAGCGTAAA CACATTAAGA GTCTCATTGA GAAAATCCCT ACAGCCAAAC 540

CTGAGCTCTT CGCTTATCCC CTGGATTGGT CTATTGTGGA TTCTATACTG ATGGAACGTC 600

GAATTAGACC ATGGATTAAT AAGAAAATCA TAGAATATAT AGGTGAAGAA GAAGCTACAT 660

TAGTTGATTT NGTTTGTTCT AAGGTTATGG CTCATAGTNC ACCCCAGAGC ATTTTAGATG 720

ATGTTGCCAT GGTACTTGAT GAAGAAGCAG AAGTTTTTAT AGTCAAAATG TGGAGATTAT 780

TGATATATGA AACAGAAGCC AAGAAAATTG GTCTTGTGAA GTAAAACTTT TTATATTTAG 840

AGTTCCATTT CAGATTTCTT CTTTGCCACC CTTTTAAGGA CTTKGAATTT TTCTTTGTCT 900

TKGAAGACAT TGTGAGATCT GTAATTTTTT TTTTTTGTAG AAAATGTGAA TTTTTTGGTC 960

CTCTAATTTG TTGTTGCCCT GTGTACTCCC TTGGTTGTAA AGTCATCTGA ATCCTTGGTT 1020

CTCTTTATAC TCACCAGGTA CAAATTACTG GTATGTTTTA TAAGCCGCAG CTACTGTACA 1080

CAGCCTATCT GATATAATCT TGTTCTGCTG ATTTGTTTCT TGTAAATATT AAAACGACTC 1140

CCCAATTATT TTGCAGAATT GCACTTAATA TTGAAATGTA CTGTATAGGA ACCAACATGA 1200

ACAATTTTAA TTGAAAACAC CAGTCATCAA CTATTACCAC CCCCACTCTC TTTTCATCAG 1260

AAATGGCAAG CCCTTGTGAA GGCATGGAGT TTAAAATTGG AATGCAAAAA TTAGCAGACA 1320

ATCCATTCCT ACTGTATTTC TGTATGAATG TGTTTGTGAA TGTATGTGTA AAAGTCTTTC 1380

TTTTCCCTAA TTTGCTTTGG TGGGGTCCTT AAAACATTTC CCAACTAAAG AATAGAATTG 1440

TAAAGGAAAA GTGGTACTGT TCCAACCTGA AATGTCTGTT ATAATTAGGT TATTAGTTTC 1500

CCAGAGCATG GTGTTCTCGT GTCGTGAGCA ATGTGGGTTG CTAACTGTAT GGGGTTTTCT 1560

TATTAATAAG ATGGCTGCTT CAGCTTCTCT TTTAAAGGAA TGTGGATCAT AGTGATTTTT 1620

CCTTTTAATT TTATTGCTCA GAAATGAGGC ATATCCCTAA AAATCTCGGA GAGCTGTATT 1680

TAATGCATTT TTGCACTAAT TGGTCCTTAG TTTAATTCTA TTGTATCTGT TTATTTAACA 1740

AAAAATTCAT CATATCAAAA AGTGTAAGTG AAAACCCCCT TTAAAACAAA ACAAAAAAAT 1800

GAAATAAAAT TAGGCAAATT GACAGACAGT GAGAGTTTTA CAAACATGAT AGGTATTCTG 1860

CTCGGCAATT TGTAAGTTTA CATGTTATTT AAGGATAAAG GTAAATCATT CAAGGCAGTT 1920

ACCAACCACT AACTATTTGT TTTCATTTTT GTCTTGTAGA AGGTTTATAT CTTGTTTTAC 1980

CTTGGCTCAT TAGTGTTTAA AAATGTACTG ATGATGTGCT TAGAGAAATT CCTGGGGCTT 2040

TCTTCGTTGT AGATCAGAAT TTCACCAGGG AGTAAAATTA CCTGAAAACG TAAGAAGTTT 2100

TAAACAGCTT TCCACACAAA TTAGATGCAA CTGTTCCCAT GTCTGAGGTA CTTATTTAAA 2160

AGAAAGGTAA AGATTGGCCT GTTAGAAAAA GCATAATGTG AGCTTTGGAT TACTGGATTT 2220

TTTTTTTTTT TAAACACACC TGGAGAGGAC ATTTGAAAAC ACTGTTCTTA CCCTCGAACC 2280

CTGATGTGGT TCCATTATGT AAATATTTCA AATATTAAAA ATGTATATAT TTGAAAAAAA 2340

AAAAAAAAAA AAAATTCCTG CGGCCGCAAG GGAATTC 2377

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 489 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

ATTGGAGCTC CACCGCGGTG GCGGCCGCTC TAGNAACTAG TGGATCCCCC GGGCTGCAGG 60

AATTCTCGAG ATCTCCCCCA AGTAAATGAA TGAAAAAAAG AACAGCAACA ATAGAGATGA 120

TATAATAAGC CAGGCATGGA TGACCTTATA GCACCCTGTA TTTATACAGA ACCACCAGGA 180

GGATAGTCAT GACAACNATG ACACTGATCA TGATNCCAGC ATTCAGAATT GAGTNCAGGG 240

CTCTCTGGCC CACAGTCTCG GTATCTTCTG TGNATGGGGT ATAGATTARC TGTCCATCCT 300

TCCGGGNATA AAANCTGACT GACTTAATGG TANCCACGAC CACCACCCAT KCAGAGAGTC 360

ACAGGGACMA AAGAGCATGA TCAACATGCT TGGCNCCATA TTTCAATNTC ANCTCCTCAT 420

CTTCTTCCTC ATCTTNCTCC ACCACCTNCC GGGAGTTAAC CCTGGGGTCG TCCATTAGAT 480

AATGGCTCA 489

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2307 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AGGGTGCTTC AGTGTGGCTG ACACAGCAGC ATGGTCTTGA CAAGTTTTCT TCATCCTACC 60

ACAAAATCCC AGTTGGTAAT AGAGACTTTA CTCCTACCTA TCAAAACCAC AAAATGTCCC 120

ATTAGGGGGG GACATGTTGT ACATGTTAGG ATCATTCAAA TAACCAAGAT TATAAGGTGA 180

GGAAAGATGC CCCTAACTGA TTCTTTTGTC TCTCATCTTG TTGGTTCCAG GGACCGAGTG 240

GGGTCAATCT TCTGGTSSTG CCTCTCCAGG TCTCTTCCAG GCCGGTCATA GACGTACTCC 300

CTCTGAGGCC GACCGATGGT TAGAAGAGGT GTCTAAGAGC GTCCGGGCTC AGCAGCCCCA 360

GGCCTCAGCT GCTCCTCTGC AGCCAGTTCT CCAGCCTCCT CCACCCACTG CCATCTCCCA 420

GCCAGCATCA CCTTTCCAAG GGAATGCATT CCTCACCTCT CAGCCTGTGC CAGTGGGTGT 480

GGTCCCAGCC CTGCAACCAG CCTTTGTCCC TGCCCAGTCC TATCCTGTGG CCAATGGAAT 540

GCCCTATCCA GCCCCTAATG TGCCTGTGGT GGGCATCACT CCCTCCCAGA TGGTGGCCAA 600

CGTWTTTGGC ACTGCAGGCC ACCCTCAGGC TGCCCATCCC CATCAGTCAC CCAGCCTGGT 660

CAGGCAGCAG ACATTCCCTC ACTACGAGGC AAGCAGTGCT ACCACCAGTC CCTTCTTTAA 720

GCCTCCTGCT CAGCACCTCA ACGGTTCTGC AGCTTTCAAT GGTGTAGATG ATGGCAGGTT 780

GGCCTCAGCA GACAGGCATA CAGAGGTTCC TACAGGCACC TGCCCAGTGG ATCCTTTTGA 840

AGCCCAGTGG GCTGCATTAG AAAATAAGTC CAAGCAGCGT ACTAATCCCT CCCCTACCAA 900

CCCTTTCTCC AGTGACTTAC AGAAGACGTT TGAAATTGAA CTTTAAGCAA TCATTATGGC 960

TATGTATCTT GTCCATACCA GACAGGGAGC AGGGGGTAGC GGTCAAAGGA GCMAAACAGA 1020

YTTTGTCTCC TGATTAGTAC TCTTTTCACT AATCCCAAAG GTCCCAAGGA ACAAGTCCAG 1080

GCCCAGAGTA CTGTGAGGGG TGATTTTGAA AGACATGGGA AAAAGCATTC CTAGAGAAAA 1140

GCTGCCTTGC AATTAGGCTA AAGAAGTCAA GGAAATGTTG CTTTCTGTAC TCCCTCTTCC 1200

CTTACCCCCT TACAAATCTC TGGCAACAGA GAGGCAAAGT ATCTGAACAA GAATCTATAT 1260

TCCAAGCACA TTTACTGAAA TGTAAAACAC AACAGGAAGC AAAGCAATGT CCCTTTGTTT 1320

TTCAGGCCAT TCACCTGCCT CCTGTCAGTA GTGGCCTGTA TTAGAGATCA AGAAGAGTGG 1380

TTTGTGCTCA GGCTGGGAAC AGAGAGGCAC GCTATGCTGC CAGAATTCCC AGGAGGGCAT 1440

ATCAGCAACT GCCCAGCAGA GCTATATTTT GGGGGAGAAG TTGAGCTTCC ATTTTGAGTA 1500

ACAGAATAAA TATTATATAT ATCAAAAGCC AAAATCTTTA TTTTTATGCA TTTAGAATAT 1560

TTTAAATAGT TCTCAGATAT TAAGAAGTTG TATGAGTTGT AAGTAATCTT GCCAAAGGTA 1620

AAGGGGCTAG TTGTAAGAAA TTGTACATRA GATTGATTTA TCATTGATGC CTACTGAAAT 1680

AAAAAGAGGA AAGGCTGGAA GCATGCAGAC AGGATCCCTA GCTTGTTTTC TGTCAGTCAT 1740

TCATTGTAAG TAGCACATTG CAACAACAAT CATGCTTATG ACCAATACAG TCACTAGGTT 1800

GTAGTTTTTT TTAAATAAAG GAAAAGCAGT ATTGTCCTGG TTTTAAACCT ATGATGGAAT 1860

TCTAATGTCA TTATTTTAAT GGAATCAATC GAAATATGCT CTATAGAGAA TATATCTTTT 1920

ATATATTGCT GCAGTTTCCT TATGTTAATC CTTTAACACT AAGGTAACAT GACATAATCA 1980

TACCATAGAA GGGAACACAG GTTACCATAT TGGTTTGTAA TATGGGTCTT GGTGGGTTTT 2040

GTTTTATCCT TTAAATTTTG TTCCCATGAG TTTTGTGGGG ATGGGGATTC TGGTTTTATT 2100

AGCTTTGTGT GTGTCCTCTT CCCCCAAACC CCCTTTTGGT GAGAACATCC CCTTGACAGT 2160

TGCAGCCTCT TGACCTCGGA TAACAATAAG AGAGCTCATC TCATTTTTAC TTTTGAACGT 2220

TGGCGCTTAC AATCAAATGT AAGTTATATA TATTTGTACT GATGAAAATT TATAATCTGC 2280

TTTAACAAAA ATAAATGTTC ATGGTAG 2307

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 343 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GGCAGCTATT TACATGGCCT CACAGGCATC AGCTGAAAAG AGGACCCMAA AAGAAATTGG 60

AGATATTGCT GGTGTTGCTG ATGTTACAAT CAGRCAGTTC TATAGACTGA TCTATCCTCG 120

AGCCCCAGAT CTGTTCCTTA CAGACTTCMA ATTKGACACC CCAGTGGACA AACTACCACA 180

GCTATAAATT GAGGCAGYTA ACGTCMAATT CTTGANNACM AAACTTKNCC TGTTGTACAT 240

AGCCTATACM AAATGCTGGG TTGAGCCTTT CATAAGGNAA AACMNAAGAC ATGGNTACGC 300

ATTCCAGGGC TKGANTACTT ATTGCTTGGC ATTCTTGTAT GTA 343

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 363 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

AAAGGGCTAA CCAGCCACTG CACCAAAATT AGTCCTTACA TTATAATACT CTGGCCATTG 60

GAAGAGAAAA ATGGGAAAAT TCAACAATTT GAAAGACTAT GATCCCTCTG GCTCATGATC 120

TACTGACCAG AATGAAGTCC TGAAGGATTT CCTTCTGTTA TGTTATCTAC CCAGCTAATC 180

TCAAACAAGA GGAGCTGGAA AGAACAAAGC CCCATGAAGC TACCCCTAGA CCCAGAAAGC 240

CAAGAACAGG GCCAAGAAAA TGAACAGCAG ACAAGCCTGA AATAGAAGTG GNACAGACAT 300

GTGGNAAGAC CAAGTACACC CAGTTNGGTG GTAAAGATTC CGATATCAAG CTTATCGATA 360

CCG 363

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 362 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

AGTACATGGT TTCTTGNCCA CCCCASCCAC CTTTCCCCAT CTCTACCGGY TGATAGTCTC 60

TCAGNTAGTA GACCTTTTCT NGTTTAGRCA GGGCCACNTT TTTAAAAACT CCAGACGGGT 120

ACCCTCCATG TKGMAGGCGA CGTGGCCCTG GATCACTCAA CTGANTGTCA TNKGANTGGT 180

GCCCCCAGAG TGAGGACAAT GGTGNAGCCC TCCTAAGGCC CTNCCTGAGT GTCCCTCCTT 240

CATGAAGATG ATTCTGAGGN TTCCCAGGCC TNCACCCTTC TTKGAAARCC CATAGNAGTT 300

CATATGNACT NCTCTNCTAT GCTCACCAAA CTCTNCCTTC ATCATACTTG GGGGATGTGT 360

GT 362

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 475 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GTGCATGTAA TTACAGTTAC GATATATGAA ACGTACAAAA TATTATGAGT ATATAATATG 60

GGGAGACTTA ATCTAGTTTG GGGGATCAGG GCACATTTCT CTAAGAAAGT GACATTTGAA 120

TTGAGCTCTG AAGGATAAAT AGACATTACC CAGAAGAATA AAATGATGGG GAAGAAGGAG 180

GACATTTTCC GTAGATTTCC AGTGGCCCCN CTTGATCCCT TATCCACTCA TCACTNAGGA 240

GGATATTAAA TKCTATAGAA ATGGRAGRAA GACMMAAAGA GACCCTNATA TCTCGAGAGG 300

ATCCAGCMAA ATTCCAAGAG ACACAACAWT AAGAAACTNG GAAGGAAGAG AAAAGGCMMN 360

NNAGGNAAAA GAAAGACAAG GAAATTNWNN NAGNACGGAG AGAAAGAGAG AGGGAGCGTN 420

NAAGGGNACG AGAAAGGCGA GNACGGGGAC GAGAAAGGGN AAGAGNACGT AAACG 475

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 346 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GGAAATAAAT GAGATCTCAG TGGTGGTATG GATTGGACTG ATCTCTGTAA CTGTGTNTGG 60

AAAAAGGACC GGAAAATGAA AGCCAGATCC CAGTAAGGGG TAGAGAGGGG CCAAGAGAAC 120

TGAACATCTG GGCTGCCGGA GAAATCAAAG TCTAGGAAGT AAGAGGTAAG AGTGTACTAC 180

AGGGGACATA CCCCAATCTC TTGGTTCCCT CCCTCTNCCT TCCTCTCCCA GAGACCCAGG 240

TCCCTGGGAC TATNTTGGAT CTGTCTCTGA AGCTGAAAAA CAAAAGGCAG AGGAGACAGT 300

CGGNTCTAAG TGACCAATCT CAAGCCAGCT TGGTCAGAAN TCCTAA 346

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 433 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

AAATCCAGTG CAGGCAACAT TATGTGGAAA TAGAAACAGG GCTCCTGCTA GGAGATTGAN 60

ATTCTGGCTT TCCTTTGGAA CCCCTCACTG ACTCATCGCC CCTGAANCAG GANCCANCAG 120

GTNCCAAGGC TCCCCTGCTC CTNTCCCTNC CCCAGGGCGA GATAGGAARC CGGAARCCTG 180

GGCAGGCTGA RCCCANCCGA CTGGAACCAG GGNAGANCCT GTGGGTGGGT GGNAGGGAGG 240

GAAGGAGGCC AGATTCCTCC AGAACTGGGG RAGAGAACAG GTTTTGGAAG TTGGGGGAGG 300

GTTTGGGTTT CACAGTGATG GTTTCATGAN ACCCTGGAGG GTTNCACACT CCTGGTKCAN 360

TTTTGNTANT CGTNCTTTGA ANACARNCCG CTTCCTTTCA ACCCTCCNCN TAAAAAGTTT 420

TGATNTTTTA AGG 433

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 350 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

ACCAAGAGCC CCCAGTTTAT GNTAACTCTC ATGACAAACA CAATTTTAGT ACCTCTCACT 60

ACCAACTATC CAGGAACCAG GANTCACCTA TTACTACGGT TCCAGCAGAA TGGGAATCCC 120

ATTCTCGGAT ATCCAGGGTA AATCCCTGAC CATGTGAGAG GAATCCTAGT GCCCCAACAA 180

CCTCACCCCC TGACTCCTCC TCAANGGCTC TGCCAAGTCA ACAAAAAAAT CCTCTACATT 240

TACACTATCT GTAAAGCCAA AGACCAGCGT CAACCTAAAT GTCCATCAAT AAGGGAATGG 300

TTGGATAAGT AAAAATTATG CAGCTGTAGG AAGGAATGAA GAATGTCTAT 350

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 512 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

AAAGGGAACA AAAGCTGGTA CCGGGCCCCC CCTCGAGGTC GACGGTATCG ATAAGCTGGA 60

TATCGAATCC TCGAGATCTA CCTAAAAAAA AAAAATTAAC TTCCCAAATG TGGGAGTCTA 120

CTCTGTTCCC TCCTNGTNTT TATTNCTGTN TACTTTYCTA ANATGGTTAA AATGTGTAAN 180

CAATATGTGT CCTTTNACTN KGGKGTGAAC ATTTTTYCTA TTATAAATYC TWAGAAAATA 240

TTNCTATGGN TATGAGATAT TKGATTCCAA GTGCCTKGTA ATTTACTYCT CAAATGTCCC 300

TGATGTKGGA NATTKGTTNC TAGTGTTYCA CTATTTAAAA AAACAGNAAT ATCTGTCTNT 360

ATGCTNAGAG CTTNTYCAGT TTYCAAATTA TTNCCTTAGG GTAAAATCCT AGAAGTAGAA 420

TTTTTGGGGC AAATTATCTA CATATTTATA ATTGTCTTGG TATTCCAAAT CTCGTTTTCC 480

AAAAGCTTAT ATCAATTTGT ACTTAACACC AG 512

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 450 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

ATTTAAGATG ACTGGGGGTC TCTNCCTAAT CCCATACTCC ACTGGAGAGG ANAAGTGGGA 60

AAGGTTGGTC TAGTTARGGT NGNTGGGGAC CCTCCCAAGA GCTGNAGAAG CAGAGATAAG 120

NAGAGCCTNC TNCTAAATCC ACATGGNCCT YCCAAGGNTC TCATCCTCTA GGACCTACCA 180

CTNCTCAGTC TACTTACTTG TCTYCTGANA TGCTTTCTNG AGGGGNAGAA AACAAAGGAA 240

GAGTAATAAC AAGCAGNAGA AACTGCAGAG AATGNAAAAT AAGTCCATAG GAGAATGTTG 300

NAAATAGAAT CATCCNCCTT TACATATTGT CACTCCAGGA AAACTGCCAA GAACCACTCA 360

TTCCTCTAGA TACAMTTCCT GTAGGATCCY CCCAGACTTC CTCCCTTAAG CACGTCAGTA 420

TTCTCCTTAT TCTCCCTTCA TTTCAACCCT 450

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 766 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

CGAGATCTGC CCCAGCCCAC ATTTCCTTTG TTGAATGAGT AGAGAAGACT GAGAAGTATC 60

ACTCACCCGT GATGTGGTTT GTCCCTTTTC CAGCCAGTGT GTTGGTAATA AAAGTCACCT 120

TTCAGAGCTT TGGTCCCCGT AATGCCCGTC TTTCCTGTGT CCAGGAATAA CCTTTGNTAC 180

TAGGCAGTCC TCTGAAAGAT TTGTAGAAGG TTAAAGTGGA AAGGGACTTG GAAGCTCATA 240

GAATCCATGC CTCTTCTTTT AGCATCAAGG AATTAGAAGT CCTGAGAGAT GAAGAATGTT 300

GTCTTCCCAA CTCAAACCCA TTTCTTGAAG CCATTTCCCT GGTTACTGNA TTGGCCACAA 360

CCCTTCCCCC TTGNTATCCT CATCCTGCTA ATGCTGTTTT TAATGGCCTG CCAGTCTGGA 420

TTTGTCTTTG GCAACCAAAC AATTTTGCTT CACAAGATTC CTACTTAAGG GAAGAGAGGG 480

GCTCCTCATT TNTCACTTGT ACAAGAGCAG GGCTGGTCAG CTTTACACAG GTGTCAGATG 540

AACCGTCACA ANCCAGANTT NCATGTTGGC CTCAGGAGGG CTTCNAGGTC CAACATCTCG 600

ACGTAAGGAG CGTTCCCAGT TCTTTCATGC TCAGATAACA GTNCTAACTN CAGCTGTTTC 660

ATCCCNAATC CCTANTTGAG GTCTTAACAT CTATTCCATT TTKCCNACMA GGGTTATNCT 720

GTTAACCCTC TNCACCAGAN TTAGANCTGA CTGATNCACT TCCTAG 766

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 327 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

TCATACTTGT ATAGTTCKNT AAGATAATCA CTCTCTCACT CAGACATNNG GNGRARNGCC 60

CNTCGATCAC TTGGGANAGG NGACTTGCMA TGTTTAATGA TTGTCANCCM NANAANTAAG 120

CTNACAGGGC AAAAACAGCC TYANGTCAGT TCTNTCTCCC TAATCCTCTA GRAKNAAATC 180

NNAWRNTRNN ACTCTGNNTC TGTGCCATNA NANATNTTNC ANTTGTATTT ATGNACTCCA 240

CATNGAGTAC ACCTCACTAA WTNTNCTNCT GGGNAACNCC CSCMCCANTT TTTNNTTGNT 300

GANANACARC AATGCTGGCA TACNGTG 327

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 431 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CCAGACTTTC ATAACTNGTG TTATTATGAA GATTAGAGTN CTGAAGCTTA CTGGATTAGA 60

AGAGNACGAG GGGGTAGCTG CCCCAATATA TTCTAATTTC TCTKGAGGAC CACCAAATNG 120

GMAGAGTGTC TCTGATAGGG AAAAGGAAGA GTTGGAAGGN ATCTTAGCCT CTAGGANAAA 180

AGAACCATTT TTATTGGCCA CCAAAGTTAC ATCTAGTKGC CTACAAATTT ATNTCCAAAC 240

TCCTTATCCT GCCAATTCAG GGTCCTGNAA ACTGATGCCA AACTATAGTT TAGTCTNCTA 300

TCACATGACT GCATTATACA TACCCAATTA TCTGGGMAAA CAGACCTGAT CCAAACACAG 360

TTKGGTNCTT TCCTTNCCTT NCCTTKGTTT AGCCTGTYCC GTCTACTNGG GGTGTCTTKG 420

ATTTGCTCCA G 431

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 276 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

TTTTTTTCCA CCAGACTTAC CAAATTTTAG ATGNATGGAA GAACTGTAAA TNCCCATAAA 60

GNTAATCTAT NCATNGACCC CCACCATTAT GATAGAGATC ATNTGGTGAN TAATGAAAGA 120

TGAAACTCTC AGCTGGGAAA GTAANAAGGA ATAGGATGTA AGTATGAGCT CCTGTTTTTT 180

ATTATNTTTA TGGATGCCCC CTCAGAAAAA TATGNAANGG GGTAACTGAC TNGGAAATGG 240

GTNTTTTATG NATAGTAAGT CCCACTCACG AGGTTT 276

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 270 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

TCGAGATCTA AAGCAGATGN AGACTTTNCA CNAAATAAAT TTACTGCTTT TTTYCTGTGA 60

NATAAGTTNC GAGAAGGAAA GCTTTKGATT NCTRNATGAG TYCAGTGGAT TATYCTNAGN 120

ACTAGAGTKG NKGTKGAAGN CATGGNACAT TTATATAGWT YWTTCAGTTC TACACTAAAT 180

GATGGAAGAA TGAGAAATCC TATATGACAA ATAGAAAAGT YCATYCTYCA TAATTGAGAA 240

CATTGAGCAG TTGGATTACC AAGATCTCGA 270

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 580 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CTTAGTTTTA GACTAGTTTC ATTATACTAC CAGTTTCTAA TATGTTGGTT TTTTATTCAC 60

TATTTGATAT ATTTGTTTTA ATATATGTTC TTGTTTTAGC AGGTAAAAGA ATCATAACAA 120

ATGTTTTTAA AAGAACATTA TTATTCTTTA ATAACTGTCT TTTTATGCAT TTGGCATGCC 180

AACTTTTTTC ATTAACATCT TGGGTATTTT ATAAAAAGAG GGAAAGCTCA ATGTTTAACA 240

GGTAGCTTTT CTTAGGAGCT AAATTAAATA TTTAACAAAT CTCCTTCCCT TCNCCCTTCC 300

CCATCCCTCA AAGNATGGGT GNANTTATCT TTAACTTTTG GGCTNGCATC CNTGNAAGCT 360

TATGGNTANT CATAGTCTNA CMAAACTAGG GTCACCNAAC TTGGCAGCAG AAATAATCTA 420

GTCTTACTGT GATAACTACC CAATTACTTT ATTATTTTTC CAGTTNCAGT TCCAAATGTT 480

TTGTGGNAAN AATTTTTNCT GTTTGTGATT TTCCAAGCTT AGAGGGGGAA ACCAACTTTC 540

CAGTGTTGGA GAGCACTGNA TAGTTTATGN ATTGTGTAAA 580

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 347 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

TGTTTCTTAA NACAGAAAAA AATTTACTGA TNGGACATTG TTCTAAGTGT ATTATTGTAT 60

TAAATGGATC ATTTAATTTA ATCTTCATAA CTGACATAGG AGTTGAGTAA CTTGTGTGGT 120

CAAATAGCTA GTAAGTGATG AGTAGGCTGG GCGCAGTGGC TCAAGCCTGT AATCCCAGCA 180

CTCTGGGAGG CTGAGGCAGG CAGATCACTT GAGGTCAGGA GTTTGAGACC AGCCTGGNCA 240

ACATGGNAAA ACCTCGTCTC TACTAAAAAT ACAAAAATTA GCTGGGCGTG GTGGGNGCGC 300

ACTTGTAGNC CCAGNTACTC GGAAGGCTGA GGCAGGAGGA ATCGCTT 347

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 430 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GCTCATCATG CTTCACGGGG GAGGCTGTGC GGGAAGAATG CTCCCACACA GNATAAAGAA 60

TGCTCCCGCA CAGGATAGAG AATGCCCCCG CACAGCATAG AGAAGCCCCC GCACAGCATA 120

GAGAATGCCC CCNCACAGCA TAGAGAAGCC CCCGCACAGN ATAGAGAATG CTCTTCACCT 180

CTGGGTTTTT AACCAGCCAA ACTAAAATCA CAGAGGGCAA CACATCATTT AAGATAGAAA 240

TTTCTGTATC TTTTAATTTC TTTCAAAGTA GTTTTACTTA TTTNCAGATT CTATTTCTTT 300

ACTAGAATTA AGGGATAAAA TAACAATGTG TGCATAATGA ACCCTATGAA ACAAACAAAA 360

GCTAGGTTTT NTNCATAGGT CTNCTTCCNN ATTGAATGAA CGTCTNTCCT CAAATTTANC 420

CCCCCAGGGA 430

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

CAAACCCTAT GNGAAATGGA AAGGAAACTA TTCTAAAGCA TAAAAGGTAG AAATATATAT 60

ACCACCCATC AAGAAAGATT ATTTTTGNTG AACTCAAGTC ACCAGAGTGG CTAAAGCCCA 120

GTAGAATGGA AATGATTATA TGGAAGGTGA GGCCAACGGG ACCAGAACAT ACTGTGATAG 180

ACAGNAAGGA GCTGTCTATC TTCTATTCTC CCACAGAAGG AGGTGACTAA GTCANCTGCC 240

CAAGCAATGT TATATCTGCA ATTGATGTNC AGCAGTACAA GTCTGAACAA CTTGGATTGG 300

NTGATTAATG TCCACANTAA ACATACAAGT CNTAATAGCT ATCTCTATAT AGTCTTTGGG 360

TNTTTACAAG GCACTGNCAC ATNATCTCAC CTATTCCTCC 400

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 500 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

AGNATCCAGA ATTGAGTGNA GNGTTCTCTG GNCCACAGTC TCGGTATCTN CTGTGAAATG 60

GGGTATAGAT TCTACAATAA AACAAACACA NNGGCCCTAG GTCAGTGTTA ATGGAGATCA 120

CCANCCACAT TACCACCTCC AACACAGAAT TTTCTTTTTC TTAATNCAAT NCGTNTCTTA 180

TAAGTCACTT TNCCCCAACT CACCAATCTA GNTAAGAATT TTTACCCTGA GAAAAACAGC 240

TACACTCTAA AATTGCTNCA AAGAAAATGT CTAACATNTG GAAAGAAGGA CTTAACATGT 300

GANGNAGACA CTGGCTCCAT CTAGNGGGTG CTTTNTTTTG AAATAATTAT AATNCCNCAT 360

CAAATTTTNG GGGGNTACAG CTTATTAGGA ACTTGTTATA GAACCAGATT CTGCCACAGA 420

ANCCACGTGG GTTGACAAGT GGTTGNCAGA AGAAAGGTAA TATGGCTTAT NATTAGGGNC 480

TCNCATCTGC AGAGTAATTG 500

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 460 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

AAAATGCTTG ANNCAAATGT CATCTAGTTC CATCTCTACG ACTCTCATGG GGTCCAAAGA 60

AGAGTTTTAN TTGAGTTTTA GAATGTGAAG TTGTGAAGTG TCTGAAAAAC TACATGGTGN 120

TCTGAAAGNC AAACTTTTAG CCTTGGGGGA GAGCATCTAA GACAGNAGGT GAAGGGNAGG 180

GGTTAGAACT AGAGGGATTG AAGAATATTA TCCATATAGG TTAGGGTTAG GTNNGGCAAC 240

GTTTTATAGA ACAAACATTG GCAAGCTACA GCCACAGGCC AGATCTGTCT NCTACCTTCC 300

CACAAAGGTG TAATAACAAA GTTATTCACA AATGTGTGAA TAAACTNNCA TTGGAAAGTG 360

CCCACGCTCC TNGGTTTATA CATTGTCTGT GGCTGCTTTC ACACTACAGT AGCACAGGTG 420

AGTGTNTGCA CTGGAGACCA TATGCCCCAT AGAGCTTTAA 460

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 370 base pairs
(B) TYPE: nucleic acid

///

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

ATCAAGCAAC AGTGTGTTAT GCCTATACTC CATGTTTATA TGTGTGTATT AAAAAATGTA 60

TTTGTATATA TGTGTATGTA TAAGTGTGTG TGTGTGTATG ATGATTCTNC TCCCGNTTTG 120

AAGGTGAAAG AAAGCACACC TTTATTTAAG CATAAACTTT GGGTTTCAGA TACTGTCTGG 180

AAAAATGATT TATCTCCCAC TTTGAAATTC CAAAATACGT ACATATATTT TTTTTTTCTT 240

TTCTTTTTTA GTTTNAGGGT CTTGCTGTGT TGCCCAGGCT GGAGTGCAGT AGTGTGATCA 300

TAGNTCACAC AGNCTCTAAC TCCCAGGNTC AAGNTATCTT CCTGCCCCAG NCTCCTGAGT 360

AGNTGGGACT 370

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 500 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

CAAAAAATCA AAGGGAAGNT GGAACCCCTG CCCACCTCTC CATTCCCCAT TCTGCTGGTG 60

GTGNCTGCTC TTCCTCACAG TACCTCCTGA AAAGTTCAGA ATTCAGTTAA TACAGAATTA 120

TTGGGTTGAT TTTCAACGTG TAGTTTAAGA TGAAGAGTTC CGNTTGGTTT AAACCACTTC 180

ACCTAACCTC TTGGTAACGG TAGTCCTGAG AGTTCGCAGT GTCANTGAAA ATCGTCCTGT 240

GACCACGCGT CAAGCTGCTG ATGGGGGACA GAAACTTCCG GGNCTATCAT ATCTCCTTGA 300

NCTCGGCCCT CAAATCTGGT AGTTTCTGCA CCGAGGGACA CAGTCCACTG CGATGAAGTA 360

TGTTCAAAAT CGNTTTCTTT AGGGAACTCC TTCCAAAGTC CAATAGTGNA AGGTGGTCAA 420

GGAAGGATTT GGAAGGAAGN TGNAAAAGTC AGNCGGGAAT CTTGATTTGG NTAGNTGTGG 480

ANANAGGAAA TCACTTGGCC 500

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 105 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GGAAAGAGGT CTCCTAACAC CCAGACAGTG TAAAAATCCA GTTTTTCTTC CTTTTGGNNG 60

GAGACAGAGT CTCGCACTGT AGCTCAGGCT GGAGTGCAGT GGCAC 105

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 386 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

AGTCCCAGCT ACTCAGGAGG CTGGGGCAGG AAGATAGCTT GAGCCTGGGA GTTAGAGGCT 60

GTGTGAGCTA TGATCACACT ACTGCACTCC AGCCTGGGCA ACACAGCAAG ACCCTAAAAC 120

TAAAAAAGAA AAGAAAAAAA AAATATATGT ACGTATTTTG GAATTTCAAA GTGGGAGATA 180

AATCATTTTT CCAGACAGTA TCTGAAACCC AAAGTTTATG CTTAAATAAA GGTGTGCTTT 240

CTTTCACCTT CAAAGCGGGA GAAGAATCAT CATACACACA CACACACTTA TACATACACA 300

TATATACAAA ATACATTTTT TAATACACAC ATATAAACAT GGAGTATAGG CATAACACAC 360

TGTTGCTTGA TAAAATATAG GGATCC 386

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 377 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

TATATTTNAT CAAGCAACAG TGTGTTATGC CTATACTCCA TGTTTATATG TGTGTATTAA 60

AAAATGTATT TGTATATATG TGTATGTATA AGTGTGTGTG TGTGTATGAT GATTCTCCTC 120

CCGNTTGAAG GTGAAAGAAA GCACACCTTT ATTTAAGCAT AAACTTTGGG TTTCAGATAC 180

TGTCTGGAAA AATGATTTAT CTCCCACTTT GAAATTCCAA AATACGTACA TATATTTTTT 240

TTTTCTTTTC TTTTTTAGTT TNAGGGTCTT GCTGTGTTGC CCAGGCTGGA GTGCAGTAGT 300

GTGATCATAG NTCACACAGG CTCTAACTCC CAGGNTCAAG CTATCTTCCT GCCCCAGNCT 360

CCTGAGTAGG TGGGACT 377

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 521 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

CTGCAGTAAG CCACGTTCAT GCCACTGTAC TCTAGCGTGG ATGACAGAGA GAGATCCTGT 60

CTTTGGAAGA AAAAAACAAA AAGAAAAAAA AAAGAGTATG GCCATGGCCT TATAATATAG 120

AAGGGGTCAC ATATTAATCT CTGAAAATGG ATCTCTTGTG GGCTTTCATA CAAGGCAACA 180

GCCACAGAGT ACGTACCTGA AAGCTGCCTG GGNTTAATGG CTGGNAGTAT GTTCTAACTN 240

GTTCAGGNAC CCATGTCACN ACTGGTGGTT ACAGAATGTG AATCTCACAC TGTCCNAAAT 300

CGGTTTTATT TTTAAAANGA ATAATTCTAN TACATTACCT TATAAAAAGT AGGTAACCTA 360

ATTTTGGNTT TTAAAAGTGA ATTGAGGGCA GATGCAAGTG GNTCACACCT ATTAATCCCA 420

AATACCTTGG AGAGGGCAAG GTAGGAGGAT TGGTTGGAGC CCAGGAGTCC AAAGACCAGG 480

CTAGGGAATA TTGNAAGAAN GTCCTCTCTA CAANAAANAA T 521

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 516 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

CTGCANGAAG CTTTTNTTNC TTTTNGGNGG AGACAGAGTC TTGCTGTGTC ANCCCAGGCT 60

GGGGTGCAGT GGNACAGTCA TAGCTCACTG CAACCTTGAA CTCCCTGGNT CATGCGATCC 120

TCCCACTTCA GCCTCTCAAG TAGCTAGAAC TACAGGTGTG CACCACCATG CCTGACTAAC 180

TTGTTTATTN GNGGGAGAGA GAACGNTCTT GCTATATTGC CTAGGCTGGT CNTTGAACTC 240

TTGGGNTNCA AGCAATCCTC CTACCTTGGC CTCTNCAAGG TANTTGGGAT TNATAGGTGT 300

GAGCCACNTG CATCTGGCCT CAATTCACTT TTAAAATNCA AAATTAGGTT ACCTACTTTT 360

TATAAGGTAA TGTATTAGAA TTATTCTTNN NAAAAATAAA ACCGATTTGG GAAAGNGTGA 420

GANTCACATT CTGTAACCAC CAGTGGTGAA ATGGGTCCCC GAACAAGGTA GAACATACTC 480

CCAGCCATTA ACCCCAGGGA GNGTTCAAGT CCGTNC 516

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 505 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GGATCCTGTT TCTTAAAACA GAAAAAAATT TACTGATAGN ACATTGTTCT AAGTGTATTA 60

TTGTATTAAA TGGATCATTT AATTTAATCT TCATAACTGA CATAGGAGTT GAGTAACTTG 120

TGTGGTCAAA TAGCTAGTAA GTGATGAGTA GGCTGGGCGC AGTGGNTCAA GCCTGTAATC 180

CCAGCACTCT GGGAGGCTGA GGCAGGCAGA TCACTTGAGG TCAGGAGTTT GAGACCAGCC 240

TGGCCAACAT GGNAAAACCT CGTCTCTACT AAAAATACAA AAATTAGCTG GGCGTGGTGG 300

GTGCGCACTT GTAGTCCCAG CTACTCGGAA GGGTTGAGGC AGGAGGAATC GCTTGGTCCC 360

CGGGAGGGAG AGGTTGNTNG TGNAGCTGAG ATCACGCCAC TNGCACTCCA GGCTGGGNAA 420

CAAAAGGGAG ACCTTTNCTC AAAAAAAAAT NAAAATAAAA AGTGATGAGT AGGATTGGGA 480

CCCNAGACAT CTTTTCTCCA AGACC 505

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 500 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

CTGCAGNCTC AAACCCTTGT CCTGGGATCA AACAATCCTC CCACCTCAGC CTTCAAAGTA 60

GATAGAACTA CAGGCATGCA CTACCATGCC TAATTTTTTA AAAAAAAATT TTTTTTCAGA 120

GATGAGATCT CACTGTGTTT CCCAGGNTTG TCCGGAACTC CTGGACTCAA GCGATCCTCC 180

CACCTTGGGC TGCCAAAGTG TTGGGATTAC AGGCATGAGC CACCATGCCT GGCCATACAC 240

TTTTTTTTTT TTTTTAANCA AGACGGAGTC TNGTTCTGTC GCCCAGACTG GAGTGCAGGG 300

GCGTNNATCT TGGCTCACTT GAAAGCTTCG CCTCCCAGGG TTCATGCCGT TCTCCTGNCT 360

CAGCCTCCCA AGTNGGTGGG ACTACAGGNA TCTGCACCAC GNCCGGTTAT TTNTTGGGTT 420

TGNNGNAGGG ACGGGGTTTC ACCATGTTAG GCAGGATGAC TTCGGACTTC CNGACCCAAG 480

ATCACCCTGC TCGGCTCCCA 500

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 440 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

GAATTCCAGA CGAGCCTGGG CAACACAGTG AGACTCTATC ACTACAAAAA AATTTTAAAA 60

TTAGCTAAAG TTGATGGNAC ATGCCTGCAG TCCCAGCTAC TCAGGAGGCT GGGGCAGGAA 120

GATAGCTTGA GCCTGGGAGT TAGAGGCTGT GTGAGCTATG ATCACACTAC TGCACTCCAG 180

CCTGGGCAAC ACAGCAAGAC CCTAAAACTA AAAAAGAAAA GAAAAAAAAA ATATATGTAC 240

GTNTTTGGGG AATTTCAAAG TGGGAGATAA ATCATTTTTC CAGACAGTNT CTTGAAACCC 300

AAAGTTTATG CTTAAATAAA GGTGTGCTTT CTTTCACCTT CAAANGCGGG AGAAGGATCA 360

TCATNCACAC ACACACACTN ATCATNCACA TTTTTACAAA TNCAATTNNN NAATACAACA 420

CATTTTAACA TGGGGTTTTG 440

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 513 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

GGATCCTGTT TCTTAAAACA GAAAAAAATT TACTGATAGN ACATTGTTCT AAGTGTATTA 60

TTGTATTAAA TGGATCATTT AATTTAATCT TCATAACTGA CATAGGAGTT GAGTAACTTG 120

TGTGGTCAAA TAGCTAGTAA GTGATGAGTA GGCTGGGCGC AGTGGCTCAA GCCTGTAATC 180

CCAGCACTCT GGGAGGCTGA GGCAGGCAGA TCACTTGAGG TCAGGAGTTT GAGACCAGCC 240

TGGCCAACAT GGNAAAACCT CGTCTCTACT AAAAATACAA AAATTAGCTG GGCGTGGTGG 300

NTGCGCACTT GTAGTCCCAG CTACTCGGAA GGCTNGAGGC AGGAGGAATC GCTTGATCCC 360

NGGGAGGGAG AGGTTGGTNG TGANGCTGAG ATCACGNCAC TTGNACTCCA GNCTGGGNAA 420

CAAANGNGAG ATCTTNTCTC AAAAAAAAAT AAAANTAAAA NGTGATGAGT AGGATTTGGA 480

CCCCAGACAT CCTNTCTCCA GGACCTGGNA TTC 513

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 390 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

GAATTCCTGG NCTCAAGTGA TCCTCTCACC TCAGCCTCCC AAATTGCTGG GATTAGAGTG 60

TGAGCCACTG TGCCTAGCCT GCATATATCT ATTTTTAATG ACTGCTAAAT CTCATTGTAT 120

GAAAATTTAT GTCCTAGCTA TAAAATTTGN TAGCACATGT TTAATTTTTT CTAATTTCAG 180

ATGTTTTAAA CTAATATTTC CCAAAGTATA GTATGGCATT TTAGGTATGA TATGATCTTT 240

NNTCCTCTTC GTACTCATTT TTATAGTTAT GGCCTGTGCA ACTGGTTTCC CATTTATATG 300

AATGATACAG AGCTTCCTAT TAAGAAAAAG TTCAGCTTGG GGAAAAAAAA AGTGAATTGT 360

CAACTTNGAG GGAAAAAAGT GAATTATTGG 390

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 366 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

TCAAGTACCT CCCTGAATGG ACTGCGTGGC TCATCTTGGC TGTGATTTCA GTATATGGTA 60

AAACCCAAGA CTGATAATTT GTTTGTCACA GGAATGCCCC ACTGGAGTGT TTTCTTTCCT 120

CATCTCTTTA TCTTGATTTA GAGAAAATGG TAACGTGTAC ATCCCATAAC TCTTCAGTAA 180

ATCATTAATT AGCTATAGTA ACTTTTTCAT TTGAAGATTT CGGCTGGGCA TGGTAGCTCA 240

TGCCTGTAAT CTTAGCACTT TGGGAGGCTG AGGCGGGCAG ATCACCTAAG CCCAGAGTTC 300

AAGACCAGCC TGGGCAACAT GGCAAAACCT CGTATCTACA GAAAATACAA AAATTNGNCG 360

GGNATG 366

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 498 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

AACACCAGGG NCATGAGGGC ACTAATCATA ATGAGATATG CCTGCTGGAG TCGAAGTGGA 60

CCTTTCCAGT GAATGGAAAT CATTCCCACC ACACCAAAAT TCCAGATCAG GAGTGNAACA 120

GTAATGTAGT CCACAGCAAC GTTATAGGTT TTAAACACTT CCCTGAAAAA AAATTACACA 180

GATTTTAAAA GATGTACAAT AATTTCCACC AAAACATTAT TTAGAATAAT GTGATGGCTC 240

CCAAACATTA GATATTAATN TCCCACCTTT ATAATTTTAC CATAACCTAT ATCAACTGTG 300

CTATTATTTA TTTAATNCTT CCCTNTAAAT TAATTTACTC TTTTTTTGTT TTTGTTTTTG 360

NGTTTGGAGC CAGTGTCTCA TTTTGGTTGC CCAGGCTTGG AGTAAAGTGG GTGCAATCAC 420

GGCTCAACTG NAGTCTTTNC CTCCNGGAGA TCAGGTNGGT CTTCCCCAGG TCCAANCTCC 480

TAAGTTGGTT NGGANAAC 498

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 469 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

TAAACAACAG GGNCATGAGG GCACTAATCA TAATGAGATA TGCCTGCTGG AGTCGAAGTG 60

GACCTTTCCA GTGAATGGAA ATCATTCCCA CCACACCAAA ATTCCAGATC AGGAGTGAAA 120

CAGTAATGTA GTCCACAGCA ACGTTATAGG TTTTAAACAC TTCCCTGAAA AAAAATTACA 180

CAGATTTTAA AAGATGTACA ATAATTTCCA CCAAAACATT ATTTAGAATA ATGTGATGGC 240

TCCCAAACAT TAGATATTAA TNTCCCACCT TTATAATTTT ACCATAACCT ATATCAACTG 300

TGCTATTATT TATTTAATNC TTCCCTCTAA ATTAATTTAC TCTTTTTTTG TTTTTGTTTT 360

TGTGTTTGGA GCCAGTGTCT CATTTTGGTT GCCCAGGCTT GGAGTAAAGT GGGTGCAATC 420

ACGGCTCAAC TGNAGTCTTT ACCTCCCGGA GATCANGTTG GTCTTTCCC 469

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 370 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

GTTTATCAAG TACCTCCCTG AATGGACTGN GTGGCTCATC TTGGCTGTGA TTTCAGTATA 60

TGGTAAAACC CAAGACTGAT AATTTGTTTG TCACAGGAAT GCCCCACTGG AGTGTTTTCT 120

TTCCTCATCT CTTTATCTTG ATTTAGAGAA AATGGTAACG TGTACATCCC ATAACTCTTC 180

AGTAAATCAT TAATTAGCTA TAGTAACTTT TTCATTTGAA GATTTCGGCT GGGCATGGTA 240

GCTCATGCCT GTAATCTTAG CACTTTGGGA GGCTGAGGCG GGCAGATCAC CTAAGCCCAG 300

AGTTCAAGAC CAGCCTGGGC AACATGGCAA AACCTCGTAT CTACAGAAAA TACAAAAATT 360

AGCCNGGNAT 370

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 316 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

GTCATGGTGT TGGCGGGGAG TGTCTTTTAG CATGCTAATG TATTATAATT AGCGTATAGT 60

GAGCAGTGAG GATAACCAGA GGTCACTCTC CTCACCATCT TGGTTTTGGT GGGTTTTGGC 120

CAGCTTCTTT ATTGCAACCA GTTTTATCAG CAAGATCTTT ATGAGCTGTA TCTTGTGCTG 180

ACTTCCTATC TCATCCCGNA ACTAAGAGTA CCTAACCTCC TGNAAATTGA AGNCCAGNAG 240

GTCTTGGCCT TATTTNACCC AGCCCCTATT CAAAATAGAG TNGTTCTTGG NCCAAACGCC 300

CCTGACACAA GGATTT 316

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 448 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

CTGCAGNCCG GGGGATCCTG GTAAAAGTCA CAAGGTCAGC CTACTAAAGC AGGGAAAACT 60

AAAGGCAAGT AAACACGTGC AGACAAAAAA AGGGATAAAG AAAAGGAATT AAGAAACTAG 120

CATTTTTAAN GTGGGGGAGG TGAATGCTTC CCAGAATGGG TTTATATCAC TTGCTTGNGG 180

GCCTTCTGAG TGTTGGNAAC AACCTGTCAT CATCACACAT ACCTGTCATC TTTAATGGTC 240

TCCATACATT ACTAATAGAT TATACAGATG GCCATCACTT AACACTTCCA CTCACTCAAT 300

TTGTNCAACA TGCAAGGTTA CCCTCTTTTT TNGCTTACNG CCACAAAGCA TTGGANAAGG 360

TTTGTGATTT TTACTAGCCN CCACTTCATC AAATTTAAGC ATTTTCTTTT TCCTNTTAAC 420

ANCCAGGACA GGNTTNAACN AAGGAAAT 448

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 450 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

CTGCAGCTCC AAGCACCTTT TTCAAATTCA GCTTTCTGTG ATTTCAGACC ACATATGCAA 60

GGAACTATCT TACCTTAATT AATAAGACTT TAAAATCCTT GTGTCAGAGG CGTTTGGACC 120

AGAGCAACTC TATCTTGAAT AGGGGCTGGG TAAAATAAGG CCAAGACCTA CTGGGCTGCA 180

TTTGCAGGAG GTTAGGTACT CTTAGTTACG GGATGAGATA GGAAGTCAGC ACAAGATACA 240

GCTCATAAAG GATCTTGCTG ATAAAACTGG TTGCAATAAA GAAGCTGGNC AAAACCCACC 300

AAAACCAAGA TGGTGAGGAG AGTGACCTCT GGTTATCCTC ACTGNTCACT ATACGNTAAT 360

TATTATACAT TAGCATGCTA AAAGACACTC CCCGCAACAA CCATGANAGG TTTACAAGTT 420

NCCATGGNAA CGNNCCCGGA NGNTANCTTG 450

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 388 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

CTGNAGCCTC CACCACCCAG GTTCAGGTGA TTCTCCTGCC GTAGNCTCAT GAGTAGNTGG 60

GATTACAGGC ATGTGCCACC ATGCCCGACT AATTTTTATA TTTTTAGTAG AGACGGGGTT 120

TCACCATGTT GGGCAGGCTG GTCTCAAACT CCTGACCTCA AGTGATCTGC CCACCTTGGC 180

CTCCCAAAGT GCTGGGATTT CAGGCGCCTG GCCTGTTACT TGATTATATG CTAAACAAGG 240

GGTGGATTAT TCATGAGTTT TCTGGGAAAG AGGTGGGCAA TTCCCGGAAC TGAGGGATCC 300

CTCCCCTTNN NAGACCATAC AAGGTAACTT CCGGACGTTG GCATGGNATC TTGTTAAACT 360

TGTCATGGNG TTGGGGGGGA GTGTCTTT 388

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 500 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

CTGCAGAAGT ATGTTTCCTG TATGGTATTA CTGGATAGGG CTGAAGTTAT GCTGAATTGA 60

ACACATAAAT TCTTTTCCAC CTCAGGGNCA TTGGGCGCCC ATTGCTCTTC TGCCTAGAAT 120

ATTCTTTCCT TTTCTAACTT TGGTGGATTA AATTCCTGTC ATCCCCCTCC TCTTGGTGTT 180

ATATATAAAG TNTTGGTGCC GCAAAAGAAG TAGCACTCGA ATATAAAATT TTCCTTTTAA 240

TTCTCAGCAA GGNAAGTTAC TTCTATATAG AAGGGTGCAC CCNTACAGAT GGAACAATGG 300

CAAGCGCACA TTTGGGACAA GGGAGGGGAA AGGGTTCTTA TCCCTGACAC ACGTGGTCCC 360

NGCTGNTGTG TNCTNCCCCC ACTGANTAGG GTTAGACTGG ACAGGCTTAA ACTAATTCCA 420

ATTGGNTAAT TTAAAGAGAA TNATGGGGTG AATGCTTTGG GAGGAGTCAA GGAAGAGNAG 480

GTAGNAGGTA ACTTGAATGA 500

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 435 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

CTGCAGAGTA ATTGCAACTG GAGTTGTCTT AAGATAATGT CACATATCCA TCTTCCCCTT 60

GTTTCTCATT CACAGAAAAA CATTTTTATT CCAGGTGCCA ATATTCCCAG CCAAAAAGAC 120

TTTACTTCTG ACTCCCTTAT ATTTAGGATG GCTATGAGAA CAAGTAAGGG CAATGACTTC 180

TAGGGAGATG TGTTGTGTAT GGAACTTCTA AGGAGAGAAT TCTGCTGACA TGTCCTATGT 240

TCTTTTCTCC CCTACTCCTT CCTACTGTCA GAAATGAAGG CTAGGGCTCC AGCCTGGACC 300

CTGAAGTAAG CTAGAGGTTA GAAGCTAAAG AAGAAAGAAG GAGATTGAGT CCTTGGATGA 360

ACGTGAAGCC ACCCTACTAA TCTGGACTGN CTACCTCTGN ACTACTCTAT GAGAGAGAAA 420

GTATGTGCAT TATTT 435

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 439 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

CATGCTCTTT GTCCCTGTGA CTCTCTGCAT GGTGGTGGTC GTGGNTACCA TTAAGTCAGT 60

CAGCTTTTAT ACCCGGAAGG ATGGGCAGCT GTACGTATGA GTTTGGTTTT ATTATTCTCA 120

AAGCCAGTGT GGCTTTTCTT TACAGCATGT CATCATCACC TTGAAGGCCT CTGCATTGAA 180

GGGGCATGAC TTAGCTGGAG AGCCCATCCT CTGTGATGGT CAGGAGCAGT TGAGAGAGCG 240

AGGGGTTATT ACTTCATGTT TTAAGTGGAG AAAAGGAACA CTGCAGAAGT ATGTTTCCTG 300

TATGGTATTA CTGGATAGGG CTGAAGTTAT GCTGAATTGA ACACATAAAT TCTTTTCCAC 360

CTCAGGGGCA TTGGGCGCCC ATTGNTCTTC TGCCTAGAAT ATTCTTTCCT TTNCTNACTT 420

GGGNGGATTA AATTCCTGT 439

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 318 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

TCCATCTCTA CGACTCTCAT GGGGTCCAAA GAAGAGTTTT AATTGAGTTT TAGAATGTGN 60

AGTTGTGAAG TGTCTGAAAA ACTACATGGT GNTCTGAAAG NCAAACTTTT AGCCTTGGGG 120

GAGAGCATCT AAGACAGNAG GTGAAGGGGA GGGGTTAGAN CTAGAGGGAT TGAAGAATAT 180

TATCCATATA GGTTAGGGTT AGGTGTGGCA ACGTTTTATA GAACAAACAT TGGNAAGCTA 240

CAGACACAGG CCAGNTCTGT CTNCTACCTN TCCACAAAGG TGTNATAACA AAGTTANNCA 300

CAAATGTGTG AATAAACT 318

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 450 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

GTTGCAAAGT CATGGATTCC TTTAGGTAGC TACATTATCA ACCTTTTTGA GAATAAAATG 60

AATTGAGAGT GTTACAGTCT AATTCTATAT CACATGTAAC TTTTATTTGG ATATATCAGT 120

AATAGTGCTT TTTCNTTTTT TTTTTTTNTT TTTTTTNNTT TTNGGGGANA GAGTCTCGCT 180

CTGTCGCCAG GTTGGAGTGC AATGGTGCGA TCTTGGCTCA CTGAAAGCTC CACCNCCCGG 240

GTTCAAGTGA TTCTCCTGCC TCAGCCNCCC AAGTAGNTGG GACTACAGGG GTGCGCCACC 300

ACGCCTGGGA TAATTTTGGG NTTTTTAGTA GAGATGGCGT TTCACCANCT TGGNGCAGGC 360

TGGTCTTGGA ACTCCTGANA TCATGATCTG CCTGCCTTAG CCTCCCCAAA GTGCTGGGAT 420

TNCAGGGGTG AGCCACTGTT CCTGGGCCTC 450

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 489 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

CTGCAGNTGA GCCGTGATTG CANCCACTTT ACTCCNAGCC TGGGCAANCA AAATGAGACA 60

CTGGCTNCAA ACACAAAAAC AAAAACAAAA AAAGAGTAAA TTAATTTAAA GGGAAGTATT 120

AAATAAATAA TAGCACAGTT GATATAGGTT ATGGTAAAAT TATAAAGGTG GGATATTAAT 180

ATCTAATGTT TGGGAGCCAT CACATTATTC TAAATAATGT TTTGGTGGAA ATTATTGTAC 240

ATCTTTTAAA ATCTGTGTAA TTTTTTTTCA GGGAAGTGTT TAAAACCTAT AACGTTGCTG 300

TGGACTACAT TACTGTTGCA CTCCTGATCT GGAATTTTGG TGTGGTGGGA ATGATTTCCA 360

TTCACTGGAA AGGTCCACTT CGACTCCAGC AGGCATATCT CATTATGATT AGTGCCCTCA 420

TGGCCCTGGT GTTTATCAAG TACCNCCCTG AATGGACTGG GTGGCTCATC TTGGCTGTGA 480

TTTCAGTAT 489

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 449 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

CTGCAGNCTT GACCTCCTGG GATCAATCGA TCCTCCCACC TCAGCCTCCT AAGTAGCTGG 60

AACTACAGGT GTGCACCACC ATGCCCGGCT AATTTTTGTA TTTTCTGTAG ATACGAGGTT 120

TTGCCATGTT GCCCAGGCTG GTCTTGAACT CTGGGCTTAG GTGATCTGCC CGCCTCAGCC 180

TCCCAAAGTG CTAAGATTAC AGGCATGAGC TACCATGCCC AGCCGAAATC TTCAAATGAA 240

AAAGTTACTA TAGCTAATTA ATGATTTACT GAAGAGTTAT GGGATGTACA CGTTACCATT 300

TTCTCTAAAT CAAGATAAAG AGATGAGGAA AGAAAACACT CCAGTGGGGC ATTCCTGTGA 360

CAAACAAATT ATCAGTCTTG GGTTTTACNA TATACTGAAA TCACAGCCAA GATGAGCCAC 420

GCAGTCCATT CAGGGAGGTA CTTGATAAA 449

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 490 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

TTCTTGCCGT TCCCGACCCG AGCCTGGTGC CCCTTCCCCA TTATGATCCT TNTCGCTTCC 60

GGCGGCATCG GGATGCCCCG CGTTGCAGGC CATNCTGTCC CAGNCAGGTA GATGACGACC 120

ATCAGGGACA GCTTCAAGGA TCGCTCGCGG CTCTTACCAG CCTAACTTCG ATCATTGGAC 180

CGCTGATCGT CACGGCGATT TATCCCGCCT CGGCGAGCAC ATGGAACGGG TTGGCATGGA 240

TTGTAGGCGC CGCCCTATAC CTTGTCTGCC TCCCCCGCGT TGCGTCGCGG TGCATGGAGC 300

CGGNCCACCT CGACCTGAAT GGAANCCGGC GGCACCTCGC TAACGGATTC ACCACTCCAA 360

GAATTGGAGC CAATCAATTC TTGCGGAGAA CTGTGAATGC NCAAACCAAC CCTTGGCAGA 420

ACATATCCAT CGCGTCCGCC ATCTCCANCA GCCGCACGCG GCGCATCTCG GGCAGCGTTG 480

GGTCCTGCAG 490

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 470 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

CTGCAGTGTT TAAAAAATAA AATAAACTAA AAGTTTATTT ATGAGGAGTA CACTGCTTTC 60

TTGTAAACAC ATGTACAAGC CATATAATAG AGTTCATTTC NNACCCTAGT TACGGAAACA 120

CTAGAAAGTC TNCACCCGGC CAAGATAACA CATCTTTAGG TAAAAATAGC AAGAAATATT 180

TTATGGGTTG TTTACTTAAA TCATAGTTTT CAGGTTGGGC ACAGTGGNTC ATGCCTGTAA 240

TCCCAGCACT TTATGCGGCT GAGGCAGGCA GATCAGTTGA GGTCAGAAGT TTGAGACCAG 300

CCTGGGCAAT GTGGCAAAAC CTCATCTCCA CTAAAAATAC AAAAATTAGC CAGGCATGGT 360

GGTGCACACA TGTTAATTCC CAGCTACTTG GGAGGNTTGA GACAGGAGGG TCGCTTGGNC 420

CTAGGAGGGA AGAAGTTGNA GGGANCTTAA TGTCACTGCA CTCTAGNTTG 470

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 445 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

CACTCAATTC TGAATGCTGC CATCATGATC AGTGTCATTG TTGTCATGAC TANNCTCCTG 60

GTGGTTCTGT ATAAATACAG GTGCTATAAG GTGAGCATGA GACACAGATC TTTGNTTTCC 120

ACCCTGTTCT TCTTATGGTT GGGTATTCTT GTCACAGTAA CTTAACTGAT CTAGGAAAGA 180

AAAAATGTTT TGTCTTCTAG AGATAAGTTA ATTTTTAGTT TTCTTCCTCC TCACTGTGGA 240

ACATTCAAAA AATACAAAAA GGAAGCCAGG TGCATGTGTA ATGCCAGGCT CAGAGGCTGA 300

GGCAGGAGGA TCGCTTGGGC CCAGGAGTTC ACAAGCAGCT TGGGCAACGT AGCAAGACCC 360

TGCCTCTATT AAAGAAAACA AAAAACAAAT ATTGGAAGTA TTTTATATGC ATGGAATCTA 420

TATGTCATGA AAAAATTAGT GTAAA 445

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 496 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

CCTGTATTTA TACTGAACCA CCAGGAGGAT AGTCATGACT ACAATGACNC TGATCATGAT 60

GGCAGCATTC AGAATTGAGT GCAGGGCTCT CTGGCCCACA GTCTCGGTAT CTTCTGTGAA 120

TGGGGTATAG ATTCTACAAT AAAACAAACA CAAAAGCCCT AGGTCAGTGT TAATGGAGAT 180

CACCAACCAC ATTACCACCT CCAACACAGA ATTTTCTTTT TCTTAATTCA ATTCGNATCT 240

TATAAGTCAC TTTTCCCCAA CTCACCAATN CTAGCTAAGA ATTTTTAACC TGAGAAAAAC 300

AGCTACACTC TAAAATTGCT TCAAAGAAAA TGTCTAACAT ATGGAAAGAA GGACTTAACA 360

TGTGAAGCAG ACACTGGCTC CATCTAGTGG GTGCTTTATA TTGAAATAAT TATAATACCT 420

CATCAAATTT TTTNGGGTAC AGNTTATTAG GAACTTGGTA TGGAACCAGA TTCTGCCACA 480

GAAACCACGN GGGCTG 496

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 496 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

CATTAGATAA TGGNTCAGGG TGGCCAAGGC TCCGTCTGTC GTTGTGCTCC TGCCGTTCTC 60

TATTGTCATT CTATAAGCAC AAGAAAAACA TTTTCAGTAA ATCAGATTCT CAGCAGAATC 120

AAGGTAACGG TTAGACCTGG GATTAACAAC AGACCCGTCA CTATGAGTTC TAAAAACCTG 180

AAGCAAGAAA AAACAATGTA CAGGAAGTAT GCAGTTTAAA AGTCTAGATT ATCTATCATT 240

GTTCACTGAA GGCATTCAGG TCCTCTCTTT TACCTGGGTC TTGGNTTGCT CCATTCTCTC 300

TGTTCATCCC AACATACACA ATTGTACTTA TCCTTTGAGA TGTACCTTAA ATACTGACAC 360

CTGCATGAAA ACTTGTTTAC TGGCTGCAGG TCCAAGCACC TTTTTCNAAA TTCAGCTTTC 420

TGTGATTTCA GACCACATAT GCAAGGAACT ATCTTACCTT AATTAATAAG ANTTTAAAAT 480

CCTTGTGTCA GAGGCG 496

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 368 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

AGGANCGCTT GGGCCCAGGA GTTCACAAGC AGCTTGGGCA ACGTAGCAAG ACCCTGCCTC 60

TATTAAAGAA AACAAAAAAC AAATATTGGA AGTATTTTAT ATGCATGGAA TCTATATGTC 120

ATGAAAAAAT TAGTGTAAAA TATATATATT ATGATTAGNT ATCAAGATTT AGTGATAATT 180

TATGTTATNN NGGGATTTCA ATGCCTTTTT AGGCCATTGT CTCAAAAAAT AAAAGCAGAA 240

AACAAAAAAA GTTGTAACTG AAAAATAAAC ATTTCCATAT AATAGCACAA TCTAAGTGGG 300

TTTTTGNTTG TTTGTTTGNT TGTTGAAGCA GGGCCTTGCC CTNCCACCCA GGNTGGAGTG 360

AAGTGCAG 368

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 500 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

GAATTCCTTT TTTTTTTTTT TTTTTTTTTT TTNCTCCTAA TGTTTTTATT GTNCCTTAGA 60

TAACTGGATA GNACAAAGTT NGNCTTNGTT TTTTACTTAA AAAACGTACT TTCCGCATAC 120

TGTNGCCCGT ATGACTTTCC TGTCCCATCG GAAACCAGAG TTTCCCCAGG TGAGCCCTTC 180

CTATCTGNGG NTACATGATT TAGCTAATTT AACAAGAAGA GAGTAATTCC TTNGGATTAT 240

TATCAACATG AAACTTGGAC TATGTCTCTA TAAGGGTGAA CACTGATTTT TTTTTTCTTT 300

TTAGAAACAA AAACCATCCA CTTATTAATC CAAACTACGG GATTGGATTT ACAACAATCA 360

TCGCATNAAC TGAACATACG AAGTTACCAC TCAAGGGAAT NACAGAAGAA CGTTGNACAA 420

TNTNTCTTAC GGGGTACGNG AATTCAAACA ATGTGGGGAN AGGAACTTCA NTCTACAAAN 480

TCTGACCATC GNTTCAGTAT 500

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 450 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

GAATTCCTTT ACTCTTCTTT AATTCTACCG TCTTTGGGCA TACATCTCAT TTGNTGTGGA 60

AGAAGGTCTG ACAGNAGGGC TGACAGCACC GATTCATAAC ACATTCTTTT CATCATACAA 120

AGAGTAAGAC CCTAGAATAA TGGGACCATC TGCTACCACG ACAGAGCTGC CTTACTGGCT 180

GTAGAAAAAG ACTGCTTGTG TGGGAGAGAA GAATGAGGAC AGAGGAGGCA TCTGGGGCAA 240

GTGAGCGTAC AAGTATNTCT ACAAATTCAG AATTTGGTGG AAAATCCAAA TTTGNCTTCA 300

ACATGATAGA GAATTGATGA GAAAATAGCT GTNCTGTTTC CAAAATTTAC TGAATTTGGG 360

AACCTGAGGT TAAAACTTTT AGGATNAAGC AACTCAGGTT CAAGACTTNG NCTNGGGAAG 420

GAATGGAAAC ACAGACGGGA ATGAGTNTCA 450

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 450 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

CAACTGTATT TATACAGNAA CCACCAGGAG GATAGTCATG ACAACAATGA CAAACTAGGA 60

ATAGCCCCCT TTCACTTCTG AGTCCCAGAG GTTACCCAAG GCACCCCTCT GACATCCGGC 120

CTGCTTCTTC TCACATGANA AAAACTAGCC CCCAGTNTGA TCCGCAGGTN GAGGAATNCC 180

CCGGGTCGAG GTTCGGATCC TGGATGACAG ACCCTCTCGC CCCTGAAGGN GATAACCGGG 240

TGTGGTACAT GGACGGNTAT CACAACAACC GCTTCGNACG TGAGTACAAG TCCATGGTTG 300

ACTTCATGAA CACGGACAAT TTCACCTCCC ACCGTCTCCC CCACCCCTGG TCGGGCACGG 360

GGNAGGTGGT CTNCAACGGT TCTTTCTNCT TCAACAAGTT CCAGAGCCAC ATCATCATCA 420

GGTTTGGACC TGAAGANAGA GAACATCCTC 450

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 500 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

GGATCCCTCC CCTTTTTAGA CCATACAAGG TAACTTCCGG ACGTTGCCAT GGCATCTGTA 60

AACTGTCATG GTGTTGGCGG GGAGTGTCTT TTAGCATGCT AATGTATTAT AATTAGCGTA 120

TAGTGAGCAG TGAGGATAAC CAGAGGTCAC TCTCCTCACC ATCTTGGTTT TGGTGGGTTT 180

TGGCCAGCTT CTTTATTGCA ACCAGTTTTA TCAGCAAGAT CTTTATGAGC TGTATCTTGT 240

GCTGACTTCC TATCTCATCC CGTAACTAAG AGTACCTAAC CTCCTGCAAA TNGCAGCCCA 300

GTAGGTCTTG GNCTTATTTT ACCCAGCCCC TATTCAAGAT AGAGTTGCTC NTGGTCCAAA 360

CGCCTCTGAC ACAAGGATTT TAAAGTCTTA TTAATTAAGG TAAGATAGGT CCTTGGATAT 420

GTGGTCTGAA ATCACAGAAA GCTGAATTTG GAAAAAGGTG CTTGGAGCTG CAGCCAGTAA 480

ACAAGTTTTC ATGCAGGTGT 500

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 500 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

CTGCAGTGAG CCAAAATCGT GCCACTGCAC TTCACTCCAG CCTGGGTGAC AGGGCAAGGC 60

CCTGCTTCAA CAAACAAACA AACAAACAAA AACCCACTTA GATTGTGCTA TTATATGGAA 120

ATGTTTATTT TTCAGTTACA ACTTTTTTTG TTTTCTGCTT TTATTTGTTG AGACAATGGC 180

CTAAAAAGGC ATTGAAATNC CAAAATAACA TAAATTATCA CTAAATCTTG ATAACTAATC 240

ATAATATATA TATTTTACAC TAATTTTTTC ATGACATATA GATTCCATGC ATATAAAATA 300

CTTCCAATAT TTGTTTTTTG TTTTCTTTAA TAGAGGCAGG GTCTTGCTAC GTTGCCCAAG 360

CTGCTTGTGA ACTCCTGGGC CCAAGCGATC CTCCTGCCTC AGCCTCTGAG CCTGGCATTA 420

CACATGCACC TGGCTTCCTT TTTGTNTTTT TTGAATGTTC CACAGTGAGG AGGAAGAAAA 480

CTNAAAATTA ACTTATCTCT 500

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 450 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

CTGCAGATGA GAGGCACTAA TTATAAGCCA TATTACCTTT CTTCTGACAA CCACTTGTCA 60

GCCCACGTGG TTTCTGTGGC AGAATCTGGT TCTATAACAA GTTCCTAATA AGCTGTAGCC 120

AAAAAAATTT GATGAGGTAT TATAATTATT TCAATATAAA GCACCCACTA GATGGAGCCA 180

GTGTCTGCTT CACATGTTAA GTCCTTCTTT CCATATGTTA GACATTTTCT TTGAAGCAAT 240

TTTAGAGTGT AGCTGTTTTT CTCAGGTTAA AAATTCTTAG CTAGGATTGG TGAGTTGGGG 300

AAAAGTGACT TATAAGATAC GAATTGAATT AAGAAAAAGA AAATTCTGTG TTGGAGGTGG 360

TAATGTGGGT GGTGATCTTC ATTAACACTG ANCTAGGGNT TTGGGGTTTG GTTTATTGTA 420

GAATCTATAC CCCATTCANA GAAGATACCG 450

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 502 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

CTGCAGCCAG TAAACAAGTT TTCATGCAGG TGTCAGTATT TAAGGTACAT CTCAAAGGAT 60

AAGTACAATT GTGTATGTTG GGATGAACAG AGAGAATGGA GCAAGCCAAG ACCCAGGTAA 120

AAGAGAGGAC CTGAATGCCT TCAGTGAACA ATGATAGATA ATCTAGACTT TTAAACTGCA 180

TACTTCCTGT ACATTGTTTT TTCTTGCTTC AGGTTTTTAG AACTCATAGT GACGGGTCTG 240

TTGTTAATCC CAGGTCTAAC CGTTACCTTG ATTCTGCTGA GAATCTGATT TACTGAAAAT 300

GTTTTTCTTG TGCTTATAGA ATGACAATAG AGAACGGCAG GAGCACAACG ACAGACGGAG 360

CCTTGGCCAC CCTGAGCCAT TATCTAATGG ACGACCCAGG GTAACTCCCG GCAGGTGGTG 420

GAGCAAGATG AGGAAGAAGA TGAGGAGCTG ACATTGAAAT ATGGCGGCNA GCATGTGATC 480

ATGCTCNTTG GCCCTGTGAN TC 502

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 499 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

CTGCAGTGTT CCTTTTCTCC ACTTAAAACA TGAAGTAATA ACCCCTCGNT CTCTCAACTG 60

CTCCTGACCA TCACAGAGGA TGGGCTCTCC AGCTAAGTCA TGCCCCTTCA ATGNAGAGGC 120

CTTCAAGGTG ATGATGACAT GCTGTAAAGA AAAGCCACAC TGGGTTTGAG AATAATAAAA 180

CAAAACTCAT ACGTACAGCT GCCCATCCTT CCGGGTATAA AAGCTGACTG ACTTAATGGT 240

AGCCACGACC ACCACCATGC AGAGAGTCAC AGGGACAAAG AGCATGATCA CATGCTTGGC 300

GNCATATTTC AATGTCAGNT CCTCATCTTC TTCCTCATCT TGNTCCACCA CCTGCCGGGA 360

GTTACCNTGG GTCGTCCATT AGATAATGGG TCAGGGTGGC CAAGGCTCCG TCTGTCGTTG 420

TGCTCCTGCC GTTCTCTATT GTCATTCTAT AAGCACAAGA AAAACATTTN CAGTAAATCA 480

GATNCTCAGC AGAATCAAG 499

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 500 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

TAACTCCCAG GNTCAAGATN TCTNCCTGCG TTAGCCTCCT GAGTAGCTGG GACTATAGGT 60

ATGTGCCACT ATTCCTGAAA ACATAATCAG TTTTGAAGGT AGTGTCTGGG CTGGGCGCAG 120

TGGNTCACGC CTTCAATCCC AGCACTTTGG GAGGNCGAGG TGGGCGGATC ACCTGAGGTC 180

AGGAGTTCGA GACCAGCCTG ACCAACATGG GATAAGACTC CATCTCTACT AAAAATACAA 240

AAAATTAGCC AGGCATGGTG GNGCATGCCT GTAATCCCAG CTACTCAGGA GGNTGAGGNA 300

GGAGAATTGG TTGGAACCTA GGAAGCAGAG GCTGTGGTGG AGCCGAGATC GCACCATTGG 360

ACTCCAGGCT GGGNAACAAG AGTGAAAATC CNTCTTAAAA AAAAAAAAAA AAAGGTAGNG 420

TTTTGNCCGG NGCGGGGGGT CACGCCTGTA ATCCCAGNAT TGGGGANGGC AAGGNGGGGG 480

GTCANNANGN NAGNAGTCCG 500

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 502 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

GAATTCTGCT GACATGTCCT ATGTTCTTTT CTCCCCTACT CCTTCCTACT GTCAGNAATG 60

AAGGGTAGGG CTCCAGCCTG GACCCTGAAG TAAGCTAGAG GTTAGAAGCT AAAGAAGAAA 120

GAAGGAGATT GAGTCCTTNG ATGAACGTGA AGCCACCGTA CTAATCTGGA CTGCCTACCT 180

CTGCACTACT CTATGAGAGA GAAAGTATGT GCATTATTTA AACCAGTTGG GTTGATTTTC 240

TATTAACAAA GTCAGAAACA TCTCTGTAAA AAGCCAGACT GAATATTTTA AGCTCTATGG 300

GTCATATGGT CTCCAGGGCA AACACTCAAC TGTGCTACTG TAGTGTGAAA GCAGGCACAG 360

ACAATGTATT AACCAAGGAG GGTGGTCACT TTCCAATGAA AGTTTATCAC AAATTGGNGA 420

ATACTTGGTA TTACACCNNG GGGGAAGGTA GGAGAAGATC TTGCCTGTGG TTGTNGNTGG 480

CAATGTTGGT CTTTTATACG NG 502

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 495 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

GAATTCTCTC CTTAGAAGTT CCATACACAA CACATCTCCC TAGAAGTCAT TGCCCTTACT 60

TGTTCTCATA GCCATCCTAA ATATAAGGGA GTCAGAAGTA AAGTCTGGNT GGCTGGGAAT 120

ATTGGCACCT GGAATAAAAA TGTTTTTCTG TGAATGAGAA ACAAGGGGAA GATGGATATG 180

TGACATTATC TTAAGACAAC TCCAGTTGCA ATTACTCTGC AGATGAGAGG CACTAATTAT 240

AAGCCATATT ACCTTTCTTC TGACAACCAC TTGTCAGCCC ACGTGGTTTC TGTGGCAGAA 300

TCTGGTTCTA TAACAAGTTC CTAATAAGCT GTAGCCAAAA AAATTTGATG AGGTATTATA 360

ATTATTTCAA TATAAAGCAC CCACTAGATG GAGCCAGTGT CTGCTTCACA TGTTAAGTCC 420

TTCTTTCCAT ATGTTAGACA TTTCTTTGAA GCAATTTTAG AGTGTAGCTG TTTCTCAGGT 480

TAAAATTCTT AGTAG 495

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 500 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

TATGGTTGCC TATTCTTGTC ACAGTAACTN AACTGATCTA GGAAAGAAAA AATGTTTTGT 60

CTTCTAGAGA TAAGTTAATT TTTAGTTTTC TTCCTCCTCA CTGTGGAACA TTCAAAAAAT 120

ACAAAAAGGA AGCCAGGTGC ATGTGTAATG CCAGGCTCAG AGGCTGAGGC AGGAGGATCG 180

CTTGGGCCCA GGAGTTCACA AGCAGCTTGG GCAACGTAGC AAGACCCTGC CTCTATTAAA 240

GAAAACAAAA AACAAATATT GGAAGTATTT TATATGCATG GAATCTATAT GTCATGAAAA 300

AATTAGTGTA AAATATATAT ATTATGATTA GTTATCAAGA TTTAGTGATA ATTTATGTTA 360

TTTTGGGATT TCAATGCCTT TTTAGGCCAT TGTCTCAAAA AAATAAAAGC AGGAAAACAA 420

AAAAAGTTGT AACTTGAAAA ATAAACATTT CCATATTTAT AGCCAACTAA GTGGGTTTNG 480

GGTNGGTTGG GTTGGTTGGT 500

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 385 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

TTATCATTAA CAGGTCCCAC AACCCTTAAA AAGTACAGAT TTTTTTTTTC TTNGTGGAGA 60

CAGGGTCTCA CTTGGTCGCC CAGACTGGAG TGCAGTGGCA CGATCTCAGT TCACCACAAC 120

CTCTGCCTCC TGGGTTCAAG CAATNCTCGT GCTTAAGCCT CCTGAGTAGG TGGAACCACG 180

CGTGCGCGCC ACCACGCTAG GTTNATTGTG GCTTTTTTAG TAGAGACAGG GTTTCGCCAT 240

GTTGCCCAGG CTGGTCTCAN ATTCCNGACC TCAAGTGATC CGNCCGCCTC AGACTCCCAA 300

AGTGNTGAGC ATTACAGNTG TGTACCACTA TGTCCCNGNC CNCATCTCTC TTTAAAACAN 360

CTTNCATTTA CCTAGTCCAC TCCTG 385

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 330 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

GACCTAGAAA AGAAAGCATT TCAANNTAAT TAACAGGTCC CACAACCCTT AAAAAGTACA 60

GATTTTTTTT TTCTTTNNGG AGACAGGGTC TCACTTTGTC GCCCAGACTG GAGTGCAGTG 120

GCACGATCTC AGCTCACCAC ANCCTCTGCC TCCTGGGTTC AAGNANTTCT CGTGCTTANG 180

CCTCCTGAGT AGGTGGAACC ACGCGTGTGC GCCACCACGC TAGGCTACTT TNTGTATTTT 240

TAGTAGAGAC AGGGTTTCGC CATNTTGCCC AGGCTGNTCT CAAATTCCTG ACCCNCAAGT 300

GATCCCCCCN CCTTCAGTAC TCCCCATCAG 330

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 382 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

GGTGGNCGTT CTAGAACTAG TGGCNCCCAA GGNAGAAGAA GTTTTCTTAG TACAGAACAA 60

AATGAAANGT CTCCCATGTC TACTTCTTTC TACACAGACA CGGCATCCAT CCGTTTTTCT 120

CANTCTTTCC NCCACCTTTC CCGTCTTTCT ATTCCACAAA GCCGNCATTG TCATCCTGGC 180

CCNTTCTCAA TGAGCTGTTG NNTACACCTC CCAGACGGCG TGGTGGNCGG TCAGAGGGGC 240

TCCTCACTTC CCAGTAGGGG TGGCCGNGCA GGNGGTGCCC CNCACCCCCC GGGCGGGGTG 300

GTTNGTCCNN CCGGNGGGNT GCACCNCCCC CACCCCTCCC CNCTCTNCTA CTGGCGGTCG 360

TNTATTNCAN NATCTTTAAG CA 382

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 360 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

GGATCCAAAG GAAGTTAGAG GCCAGCTCAG TCTACACCTG CTACTGNTCA GTGCCCACCC 60

GGTCAAGGGA GACCAACACA TGGTAAAGGT CAAGGGCTTC TTGGAAGGCA GTCAGCAGCC 120

TGTGCAAGAT GTTCTCCACA CTGCTCAGNT TAAGGGGAGC TGGGGGCAGG ACCTCAGCTG 180

GNATCTCTGC TTCACCAGTG TCCAGGGGTT GCACAATTCT TGTTTACTCG TAGGATATTT 240

AATCTTGGNN GGTGCTATCA TAAATGGGAC TTATCCNCTN ATTATGTTTT CTTACTAGTT 300

GTTTATGTGA AGGTTATTGA TTTGGGTTTC ACTTTATTTN GTGGNAATGG AGTTTCACTC 360

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 208 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

AATGTCACGG ATTCCTTTAG GTAGNTACAC CCATCAACCT TTTTGAGAAT AAAATGAATT 60

GAGAGTGTTA CAGTCTAATT CTATATCACA TGTAACTTTT ATTTGGATAT ATCAGTAATA 120

GTGCTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTNG GNGANAGAGT CTCGCTCTGT 180

CGCCAGGTTG GAGTGNAATG GTGCGATC 208

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 470 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

AACAAGGTTT CTCGGTCGGC GGTGAATATA CCGGGGCGTC GATATTTGTT GCGGAATACT 60

CCCCTGACCG TAAACGTGGC TTTATGGGCA GCTGGCTGGA CTTCGGTTCT ATTGCCGGGT 120

TTGTGCTGGG TGCGGGCGTG GTGGTGTTAA TTTCGACCAT TGTCGGCGAA GCGAACTTCC 180

TCGATTGGGG CTGGCGTATT CCGTTCTTTA TCGCTCTGCC GTTAGGGATT ATCGGGCTTT 240

ACCTGCGCCA TGCGCTGGAA GAGACTCCGG CGTTCCAGCA GNATGTCGAT AAACTGGAAC 300

AGGGCGACCG TGAAGGTTTG GAGGATGGCC CGAAAGTCTC GTTTAAAGAG ATTGGCACTA 360

AATACTGGNG CAGNCTGTTG AATGTTTGGG CTTGGTAATT GGCAACCAAC GTGATTACTA 420

NATGTTGGTG ACCTATATTG CCGAGTTATT GGCGGATAAC CTGAATTATC 470

(2) INFORMATION FOR SEQ ID NO:100:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 440 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

TAATTATATT GAAATGCTTC TCNTCTAGGT CATCCATGNC TGGNTTATTA TATCATCTCT 60

ATTGNTGNTG CTCTTTTTTA CATNCATTTA CTTGGGGTAA GTTGTGAAAT TTGGGGTCTG 120

TCTTTCAGAA TTAACTACCT NNGTGCTGTG TAGCTATCAT TTAAAGCCAT GTACTTTGNT 180

GATGAATTAC TCTGAAGTTT TAATTGTNTC CACATATAGG TCATACTTGG TATATAAAAG 240

ACTAGNCAGT ATTACTAATT GAGACATTCT TCTGTNGCTC CTNGCTTATA ATAAGTAGAA 300

CTGAAAGNAA CTTAAGACTA CAGTTAATTC TAAGCCTTTG GGGAAGGATT ATATAGCCTT 360

CTAGTAGGAA GTCTTGTGCN ATCAGAATGT TTNTAAAGAA AGGGTNTCAA GGAATNGTAT 420

AAANACCAAA AATAATTGAT 440

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 449 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

AAAACAAAGC CTCTTGAGGT TCTGAAAAGG GAAAGAAAAA CAGAACTTTG TGCACTACAA 60

TTATACTGTT ATAAAAAACA CTTCCATAGA TTACATTAAG CAGAAACAAA CCTTTCTTTC 120

ATGTGTTCTC CTCCAGGCCA AGCTGTCTAA GGACCGCAAA GGCTGTTGTC ACTTGCAGGC 180

TCCCAGATTA GGTCTGAAAT AGGATTTCAC CAGGTCATCC ATTGTTAGTT AAATCCTAGT 240

AAATTCATTT ANACCAATCA AATACTTATA AGACCAATTT GTAAACCAGG AATGTATTAA 300

TTTGTCACGA CTTTCAACTA ACTGACAAAT TTACTATAAG CTCAAGGTAG GACTCTTTAG 360

CAATAAGTAG GAACCGCCTG AGACAACCAA ACATTTTCAA CCCACAAANG ATACTTTAAT 420

GACTTTCTGA TTTNCCAGCA AAAGGGGGG 449

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 425 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

GGATCCGCCC TCCTCGGCCT CCCAAAGTGT TGGGATTACA GGCGTGAGCC ACCGCACCTG 60

GCTTTTTTTT TTTTTTTTTT TGGNGGAGAC AGAGTCTTAC TCTGTTGCCC AAGCTGGAGT 120

GCAGTGGTGC AATCTTGGTT CACTGNAACC TCCACCTCCA GAGTTCAAGC AATTCTCTGC 180

CTCAGTTTCT GGAGTAGCTG GGATTACAGG TGCCTGCCAT CACGCCTGGC TAAATTTGGN 240

ATTTTTTTTT AGTAGAGACA GGGTTTCACC ATGTTGGCCA GGCTGGTCTT GAACTCCTGA 300

CCTTGTGATC CACCAGCCTC GGCCTCCCAA ATTGNTGGGA TTACAGGCGT GAGCCACCAC 360

AACCAGGCTA AAGTTTTAAA ACATGCCAAG TGTATTTACA TAATGCGATA CGANTTATGT 420

ACATA 425

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 386 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

GGATCCGCCC GCCTTGGCCT CCCAAAGTGC TGGGATTACA GGCATGAGCC ACCGCTCCTG 60

GCTGAGTCTG CGATTTCTTG CCAGCTCTAC CCAGTTGTGT CATCTTAAGC AAGTCACTGA 120

ACTTCTCTGG ATTCCCTTCT CCTNTTGTAA AATAAGCATG TTATCTGTCC NNCCTGCCTT 180

GGGCATTGTG ATAAGGATAA GATGACATTA TAGAATNTNG CAAAATTAAA AGCGCTAGAC 240

AAATGATTTT ATGAAAATAT AAAGATTAGN TTGAGTTTGG GCCAGCATAG AAAAAGGAAT 300

GTTGAGAACA TTCCNTTAAG GATTACTCAA GCTCCCTTTG GTGTATATCA GNNGTCANNA 360

CNTATCTTNG GGGCTGAAAA ATGTTT 386

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 224 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

GAAAAGGGAA AGAAAAACAG AACTTTGTGC ACTACAATTA TACTGTTATA AAAAACACTT 60

CCATAGATTA CATTAAGCAG AAACAAACCT TTCTTTCATG TGTTCTCCTC CAGGCCAAGC 120

TGTCTAAGGA CCGCAAAGGC TGTTGTCACT TGCAGGCTCC CAGATTAGGT CTGAAATAGG 180

ATTTCACCAG GTCATCCATT GTTAGTTAAA TCCTAGTAAA TNCA 224

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 440 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

GGATCCGCCC TCCTCGGCCT CCCAAAGTGT TGGGATTACA GGCGTGAGCC ACCGCACCTG 60

GCTTTTTTTT TTTTTTTTTT TGGNGGAGAC AGAGTCTTAC TCTGTTGCCC AAGCTGGAGT 120

GCAGTGGTGC AATCTTGGTT CACTGCAACC TCCACCTCCA GAGTTCAAGC AATTCTCTGC 180

CTCAGTTTCT GGAGTAGCTG GGATTACAGG TGCCTGCCAT CACGCCTGGN TAAATTTGGG 240

ATTTTTTTTT AGTAGAGACA GGGTTTCANC ATGTTGGCCA GGNTGGTCTT GGACTCCTGA 300

CCTGGTGAAC CACCAGGCTC GGGCTCCAAA TTTGGTTGGG ATTACAGGGG GTNAANCAAC 360

CACAACCCAG NCTAAAGTTT TNAAAACATN CAAAGTGTTT TAAAATNATG NGATACGATT 420

TATTGTACAA TTAATTTTAT 440

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 448 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

GTCTTTCCCA TCTTCTCCAC AGAGTTTGTG CCTTACATTA TTACTCCTTG CCATTTTCAA 60

GAAAGCATTG TCAGCTCTTC CAATCTCCAT CACCTTTGGG CTTGTTTTCT ACTTTGCCAC 120

AGATTATCTT GTACAGCCTT TTATGGACCA ATTAGCATTC CATCAATTTT ATATCTAGCA 180

TATTTGCGGN TAGAATCCCA TGGATGTTTC TTCTTTGACT ATAACAAAAT CTGGGGAGGA 240

CAAAGGTGAT TTTCCTGTGT CCACATCTAA CAAAGTCAAG ATCCCCGGCT GGACTTTTGG 300

AGGTTCCTTC CAAGTCTTCC TGACCACCTT GCACTATTGG ACTTTGGNAA GGAGGTGCCT 360

ATAGAAAACG ATTTTGGAAC ATACTTCATC GCAGGGGGAC TGTGTCCCCC GGTGGCAGAA 420

NCTACCAAGA TTTGCGGGNC GAGGTCAA 448

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 198 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

GGATCCGCCC GCCTTGGCCT CCCAAAGTGC TGGGATTACA GGCATGAGCC ACCGCTCCTG 60

GCTGAGTCTG CGATTTCTTG CCAGCTCTAC CCAGTTGTGT CATCTTAAGC AAGTCACTGA 120

ACTTCTCTGG ATTCCCTTCT CCTTNAGTAA AATAAGNATG TTATCTGNCC GCCCTGCCTN 180

GGNNATTGNG ATAAGGAT 198

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 500 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

CTGCAGTGAG CCGTGATTGC ACCACTTTAC TCCAGCCTGG GCAACAAAAT GAGACCCTGG 60

CTCAAAAACA AAAACAAAAA CAAAAAAAGA GTAAATTAAT TTAAAGGGAA GTATTAAATA 120

AATAATAGCA CAGTTGATAT AGGTTATGGT AAAATTATAA AGGTGGGATA TTAATATCTA 180

ATGTTTGGGA GCCATCACAT TATTCTAAAT AATGTNTTGG TGAAAATTAT TGTACATCTT 240

TTAAAATCTG TGTAATTTTT TTTCAGGGAA GTGTTTAAAA CCTATAACGT TGCTGTGGAC 300

TACATTACTG TTGCACTCCT GATCTGGAAT TTTGGGTGTG GTGGGAATGA TTTCCATTCA 360

CTGGAAAGGT CCACTTCGAC TCCAGCAGGC ATATCTCATT ATGATTAGTG CCTCATGGNC 420

CTGGTGTTTA TCAAAGTACC TCCCTGAATG GACTGCGTGG GTCATCTTGG NTGTGATTCA 480

GTATATGGTA AAACCCAAGA 500

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 500 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

CTGCAGCCTT GACCTCCTGG GATCAATCGA TCCTCCCACC TCAGCCTCCT AAGTAGCTGG 60

AACTACAGGT GTGCACCACC ATGCCCGGCT AATNGNTGTA TTTTCTGTAG ATACGAGGTN 120

TNGCCATGTT GCCCAGGCTG GTCTTGAACT CTGGGCTTAG GTGATCTGCC CGCCTCAGCC 180

TCCCAAAGTG CTAAGATTAC AGGCATGAGC TACCATGCCC AGCCGAAATC TTCAAATGAA 240

AAAGTTACTA TAGCTAATTA ATGATTTACT GAAGAGTTAT GGGATGTACA CGTTACCATT 300

TTCTCTAAAT CAAGATAAAG AGATGAGGAA AGAAAACACT CCAGTGGGGC ATTCCTGTNA 360

CAAAACAAAT TATCAGTCTT GGGGTTTNAC CATATACTGA AATCACAGGC AAGATGAGCC 420

ACGCAGTCCA TNCAGGGAGG TACTGGATAA CACCAGGGNC ATGAGGGACT AATCATAATG 480

AGATATGCTG CTGGAGTCGA 500

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 550 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

CTGCAGGATG AGAGCGATCT CTTNTTNCAT TTCCTGCGCT ACGCGCTGCG GGCGACCAAA 60

TTCTTTCGCC ATAATAAATT CTCCTGACNA AAAAGGGGCT GTTAGCCCCT TTTTAAAATT 120

AATTTCAGGT GGAAGGGCTG TTCACGTTGA CCTGATAAGA CGCGCCAGCG TCACATCAGG 180

CAATCCATGC CGGATGCAGC GTAAACGCCT TATCCCGCAT GGAACCCTAA AAACCTTAAG 240

CAATGGTACG TTGGATCTCG ATGATTTCGA ATACTTCGAT CACATCGNCA GTGCGGACGT 300

CGTTGTAGTT CTTAACGCCG ATACCACATT CCATACCGTT ACGGGACTTC GTTAACGTCA 360

TCTTTGGAAG CGGGGCAGGG ACTCCAGCTC GNCTTCGTAG ATAACCACGT TGGCACGCAG 420

GAACGCGGGT CGGGTTGTGA CGTTTAACAC AACTTCCGGG TAACCATACA GGCTGNGATG 480

GNACCAAATT TCGGGGGATT TGGACAAGTC AAGAACTTCC CGCCAGACCG ATAATCTTGT 540

TGTTCAGTTC 550

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 541 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

CTGCAGCTTT CCTTTAAACT AGGAAGACTT GTTCCTATAC CCCAGTAACG ATACACTGTA 60

CACTAAGCAA ATAGCAGTCA AACCCAAATG AAATTTNTAC AGATGTTCTG TGTCATTTTA 120

TNTTGTTTAT GTTGTCTCCC CCACCCCCAC CAGTTCACCT GCCATTTATT TCATATTCAT 180

TCAACGTCTN NNTGTGTAAA AAGAGACAAA AAACATTAAA CTTTTTTCCT TCGTTAATTC 240

CTCCCTACCA CCCATTTACA AGTTTAGCCC ATACATTTTA TTAGATGTCT TTTATGTTTT 300

TCTTTTNCTA GATTTAGTGG CTGNGTTGTG TCCGAAAGGT CCACTTCGTA TTGCTGGTTG 360

AAACAGCTCA GGAGAGAAAT GAAACGCTTT TTCCAGCTCT CATTTACTCC TGTAAGTATT 420

TGGAGAATGA TATTGAATTA GTAATCAGNG TAGAATTTAT CGGGAACTTG AAGANATGTN 480

ACTATGGCAA TTTCANGGNA CTTGTCTCAT CTTAAATGAN AGNATCCCTG GACTCCTGNA 540

G 541

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 241 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

NNCCCNCNCN NNNNNNNTTN NTNTTGCCCG ATAACTATAG GGNGACTTGG AGATCCACCG 60

CGGTGGCGGN CGNTCTAGAA CTAGTGGATC CCCCGGGNTG CAGGACCCAA CGCTGCCCGA 120

GATGCGCCGC GTGCGGTTGC TGGAGATGGC GGACGCGATG GATATGTTCT GCCAAGGGTT 180

GGTTTGCGCA TTCACAGTTC TCCGCAAGAA TTGATTGGCT CCAATTCTTG GAGTGGTGAA 240

T 241

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 834 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

CCCCCCCNCC NNNNNTTTTN NGCAGCCCGT AATTACCCTC ACTNCCGGGA ACAAAAGCTG 60

GGTACCGGGC CCCCCCTCGA GGTCGACGGT ATCGATAAGC TTGATATCGA ATTCCTGCAG 120

TGTTTAAAAA ATAAAATAAA CTAAAAGTTT ATTTATGAGG AGTACACTGC TTTCTTGTAA 180

ACACATGTAC AAGCCATATA ATAGAGTTCA TTTTTTACCC TAGTTACGGA AACACTAGAA 240

AGTCTTCACC CGGCCAAGAT AACACATCTT TAGTAAAAAT AGCAAGAAAT ATTTTATGGG 300

TTGTTTACTT AAATCATAGT TTTCAGGTTG GGCACAGTGG NTCATGCCTG TAATCCCAGC 360

ACTTTATGCG GNTGAGGCAG GCAGATCAGT TGAGGTCAGA AGTTTGGAGA CCAGNCTGGG 420

CAATGTGGNA AAACCTCATC TCCACTAAAA ATACAAAAAT TAGNCAGGCA TGGTGGTGCA 480

CACATGTAAT TCCAGNTACT TGGGGAGGCT GAGACAGGAG GATCGNTTGA ACCTAGGGAG 540

GGAGGAGTTG GAGTGAGCTA ATGTCAATGC ACTCTTGGTT GGGGCGANAG AGCAAGATCT 600

TTCTTCCAAA AAAAAAAAAA AAAAAAAAGC CAGGTGNGGN GGTCAAGGCT GTAATCCAGA 660

ATTNGGGAGG CCGNGGAGGN NATCANTGNG GNAGGNGTCA AGNGGGGCNG GCCACATGGG 720

GAACCCGTTN TTNTTAAATN AAAATTAGCC GGGGNGGGGG AGGACTNTAT CCNGTTCCGG 780

NGGTGNGGAG GATCNTTATT NTGGNGGAGG GTGGATGNNC CAGTTGACNC CCCC 834

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 838 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

TTGGGCNCNC GCCCCTTAAN TTTTTATNGN TTNCTANAAA AANANNNGGC NCNNTAAAAT 60

ATATTTTTTN TTGTGACCCC TTTTAAAAGG GACCCNCTAA AAAATTTTNT GGTTNNTTTN 120

GATTTANGTG GGTGNTTTTN TTATATTTTT GGNGAGNNTC TGTAGTCNTC NCCCTCAAAC 180

ANNTCNTACN ATNGGNANCG TGACTCTGTC NTTNGTNANN NTCGNTNTCN NGTNATTCNA 240

GGNNCCTCGC GCNNCNCGGG CNNNGTTTTT TTTNNCNNTT TTTAAGCCNA ANNCTCAGTA 300

NCNTCCAACG GNGCTNNGAC ANNNGNNNCT NTCGNGGGTN CCCTCTNTNT NGNNCNNGGC 360

TNNNGNNNNC NGNCNGCNGN GCCNTGCGNN NNGNNNGNGG NNNGNTNNCA TANGGATNGN 420

GNTGCTCNNC NCNNGNGTNN TNAGTAGGNA NTTTTNTNNT ACTTGCCNNC NNNTNGCTGC 480

GAGNANAGCN ANNTNGNNGN AGNGNNGNTG CGCGGANNTT CCCCTGATNA NCTCGAGCNG 540

NTTACNGGNG CNNCCTNGAA NAAGNGNNGT ANNGTGCCGA GNCGCTANNC TGAGCCTGAG 600

TNTCGACNGG NATNGTGNNT CNTACNGTTA NGGGNNGCNN GANCGGGNTG ANTCNCCGGN 660

NGANCNAGCG ACTGCCTNTC ANGCGAANCG TNTCANGNNN GTAGAGCANA GGGTNANNNG 720

TCNNNNAAGC NTNNAGTGAN TGTCNTNACN NGTGANTTAC GGCNTAGNCT TGATNTNNAN 780

NCGAGGNNNN ATNNANNNTT GGANANTTNN TNNNNTCNCN TCGCGGNGNG NCNNGCCG 838

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 803 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

ATTCGCGCGT AGCCCGATAA CTATAGGGCG ACNTGGAGNT CCACCGCGGT GGCGGCCGCT 60

CTAGNAACTA GTGGATCCCC CGGGCTGCAG GAATTCACGG ACTAATCCTC TACAGATCTT 120

GCTGGAGTGG CCTTTCAGCC TTTTGTGACT GTTTGTAGTG AAATGTACAC ACAAGCCTAC 180

AAGGCAGCCC AGATGTACCA TAACTGTGGG AAAATTAAAA AAAAAAAAAC ACAGAACCTC 240

TCTATGTTGC CCATGCTGGA CTCAAACTCT TAGACAAGCA ATCCTCGTAC CTCAGCCTCC 300

TGAGTTCCTG AGTAGCTGGG ACTACAAGCA TGCACCACCA TGCCAGGCTA TGAGAAAGTT 360

CTTTTTATTG ATCCAGACCT TATTGCCTGG TAACTTCCAC CACTGTTCCT AGCTCTGNTC 420

TCTGGTCCTA ACAGAGGAAA ATCTTGACCC CACACCTAGT GCAACTGGAT AGCTTATNGT 480

TGGGCTNGTG TTTCCTCTAT TCTGGGTCCA CCCTAAAATC CNATAGATAC TCCAACTGCT 540

CANAGNAAAC CAAGCTCTCT CTCTNNCTTN CTTTCTTNNN CTCTATTNAT TNATGGGNNA 600

TNATTNATTN NGGGGATGGN GTTCGGTCGC CGCCCGGCTG GNGTGAAATG GGGGAGGCAA 660

TCAATTTAAC CCCACCCNGG GTCCAGGGAT CTCGTTNAAA CCGNNNNNNN NNNNNNNNNA 720

NGNNCNNCNC NNNCCNNTNN NNNGGTTTNN NNGNNNNGGG NNNCCNNNNN NANNNNNNTN 780

NNNCCNCCNA NNNTNCNNNN CCC 803

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 780 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

CNNNNNNNCC CNNTNATTNT ACGCCAGCCG CGTAATTAAC CCTCACTAAA GGGAACAAAA 60

GCTGGGTACC GGGCCCCCCC TCGAGGTCGA CGGTATCGAT AAGCTTGATA TCGAATTCCA 120

ACTCCTCACT TGCCAGATGT GACCTTAAGC AAGTGAACTT CTGTGTGCCA CACTGTTTTC 180

ATCTGTAAAA GGATAAAGGG AATATCATAA ATTAGNTTGT TAAGCCTTAG TTTAATAATG 240

TCTCTAAGTT TTACATATAA GTAGACAGTG TCTTTCTTGT TTAGTGAATA ATCATTCTTA 300

TTATTTAATA GTATCTCTAC TAAATTTATT GTGTAAGATT ATACTAATCT TGTTTAGTGC 360

GTGGTAATCA CTTCTGCTCA TATTTAACCT ATAAGCATAA TATAGTTTAT TTATATACCA 420

NTTATTTATT TTATTTTATT TGNNGAGATG CAGCTTGTCT TTTNCAACCC AGGGNTGNGG 480

NGNAGNNGNG NAANCTTGNT TCACTGNAAC CNCCACCNCC CAGGTNCAAG NGATTCTCCT 540

GNTCAAGCCN CCTNAGNAGN TGGNATTACA GNACGANTAC ANNCCAGNTA NNNNGGNTNT 600

NNGNTNGNNA GGNNNCACAN NNGNCAGGTN NNTCGNCTCC NNGCCANTNA CTNNNNCCAN 660

CCCCNNNGNN NNNNATANAG NATNANCANN NNCCNCNNNN NCNNNNNNNG GNGGANNCCN 720

NNTNGCNGNN ANNGNNANNN NNTNNNNNNN NNGGNCNNNG NNNNNNNNCC NNNNNNCCCC 780

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 803 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

NNNNNNNNNC CNNNNNNTTC GNNCGTAACN CGANTCACTA TAGGGCGACT TGGAGCTCCA 60

CCGCGGTGGC GGCCGCTCTA GAACTAGTGG ATCCCCCGGG CTGCAGGAAT TCGATATCAA 120

GCTTTNGTGT GTAAAAAGTA TTAGAATCTC ATGTTTTTGA ACAAGGTTGG CAGTGGGTTG 180

GGAGGAGGGA TTGGAGATTG ATGCGATAGG AATGTGAAGG GATAGCTTGG GGTGGATTTT 240

ATTTTTTAAT TTTAATTTTT ATTTNTTGAG ATGGAGTCTT GCTCTGTCTC CCAGGCTGGA 300

GTGCAGTGGT GTGATCTCAG CTCACGGGTT CAAGCGATTC TCCTGCTGCA GCCTCCCGAG 360

TAGCTGGGAT TACAGGAGCG CGCCACCACA CCCGGNTAAT TTNNTTGTAT TTTTAGTAGA 420

GACGGGGTTT CACCATGTTG GTTAGGCTGG TCTAGAACTC CCAACCTCAT GATCCGCCTG 480

CTTCGGCCTC CCAAAGTGCC GGAATTACAG GCGTGAGCGA CTGCACCCGG CCGCTTGGGG 540

GTGGATTTTT AAAGAAATTT AGAAGAATGT AACTTGGCCA GATACCATGT ACCCGTTAAT 600

TCATTTNCGG TTTTTTGGAT ACCCATTTTG NNATTCTCCC NCCACTGGAT AAATAAGGGN 660

GGTTCATTNT NGNTTAGTTT GGGTNTTTTT NAGTGTGGNT TCTGCTTATN ATTAGAATGG 720

NCTNCTTTNC CAANCTGGAA AGGGAGGAGT TAAAATCANT ACCAGAANCA GAAATTCTTT 780

TCANTTGTTG CNCNAGAAAT GCC 803

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 819 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

TNCCNNNNCN NNNNNAATTT TNGCAGNCGC GTAATTAACC TCACTAAAGG GAACAAAAGC 60

TGGGTACCGG GCCCCCCCTC GAGGTCGACG GTATCGATAA GCTTCCCTCC CCTTCCTCAG 120

CTCTGGCGAC CCTGCGCTGT GGTGGTTCTC CAACCACACT CATTCTCCTC AGCTGGCTCC 180

TTGCTCTTCT TCCACCCCCT CGTTGGAAGT GTTCCTAAGT GTTTGGCTTG GCCTCCTCTT 240

CCCCTTCCTT AGNTTAGACT TCTCCACTGC TCCAACATCA ACTGGAAATC TATGGAATTG 300

ATTCCTGTTT TCAGCTCCAG TCCTGTTCAC AGGGCATTTT CACCTGCTGG CACTTCCAAA 360

GTGACACTTC CAAACCACTT CCTCGCCCTC CTCTCTAAAC CAGGTCTTTC TTCCTAACTT 420

CCTTATTTCT GAGAATGTCT CTGNCATGTT CTAAACTGAA AACTCCTAGT CAACTNCACA 480

CTTTATTCCC TGGATCCTCA ATTGGGTTCC CATGTNCCGT TAGTGTTTCT TGGTAAGNCT 540

CTGCCANCAC CGNAGGATCG ACTCTAATCA CATCTCAACT GAATTATGGN AAAGTCAACT 600

CAATTCTCTC AACCATCCCA GGCTCCACTA TGGNTAATAT GCTAAGGAGA GCTGACCCAA 660

CGGGGAGAAG ATCTGNGGGG GAGGAGAGAA ACAAAGNTAA TGGAATNATT CTCGAAAAGC 720

CCACAAGGNG AAGGATAACC CNCTTCCNCT CGAAAGAGGG GGGATCGCCA GATNTCGCGC 780

CCGGAAAGAA ACCGGGGNGA GGGGGTTACA NTGTAAGNC 819

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 796 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

TNTTGGCTGG TACTGCTTGA GCAACTGGTG AAACTCCGCG CCTCACGCCC CGGGTGTGTC 60

CTTGTCCAGG GGCGACGAGC ATTCTGGGCG AAGTCCGCAC GCCTCTTGTT CGAGGCGGAA 120

GACGGGGTCT GATGCTTTCT CCTTGGTCGG GACTGTCTCG AGGCATGCAT GTCCAGTGAC 180

TCTTGTGTTT GCTGCTGCTT CCCTCTCAGA TTCTTCTCAC CGTTGTGGTC AGCTCTGCTT 240

TAGGCATATT AATCCATAGT GGAGGCTGGG ATGGGTGAGA GAATTGAGGT GACTTTTCCA 300

TAATTCAGGT GAGATGTGAT TAGAGTTCGA TCTGCGGTGG TGGCAGAGGC TTACAAGAAA 360

CACTAACGGG ACATGGGAAC CAATTGAGGA TCAGGGAATA AAGTGTGAAG TTGACTAGGA 420

GGTTTTCAGT TTAGAACATG GCAGAGACAT TCTCAGAAAT AAGGAAGTTA GGAAGAAAGA 480

CTGGTTTAGA GAGGAGGGCG ANGAAGTGGT TTGGGAAGTG TCACTTTGGG AAGTGCCAGC 540

AGGTGAAAAT GCCTGTGACA GGATGGAGCT GAAAACAGGA TCAATTCCAT AGATTCCAGT 600

TGATGTNGGA GCAGGGGAGA AGTCTTAGCT AAGGAAGGGG AAGAGGAGGC CAAGGNAACA 660

CTTAGGACAA TTGNAACGAN GGGGGGGGAG AAGAGNAAGG GCCACTTAGG GGAATAATNT 720

GGTGGGGGAC CCCCAAGNNA GGGCGCANNN TTAGGAGGGG GGGANNTCAN AGGAAAGTGG 780

AAGNTTGGGT TTANCT 796

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 802 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

ATTCGTCGTA NCCCGATNAC TATAGGGCGA CTTGGAGCTC CACCGCGGTG GCGGNCGCGG 60

GCAGGGNCCG GNCCTTTGTG GCCGCCCGGG CCGCGAAGCC GGTGTCCTAA AAGATGAGGG 120

GCGGGGCGCG GNCGGTTGGG GCTGGGGAAC CCCGTGTGGG AAACCAGGAG GGGCGGCCCG 180

TTTCTCGGGC TTCGGGCGCG GCCGGGTGGA GAGAGATTCC GGGGAGCCTT GGTCCGGAAA 240

TGCTGTTTGC TCGAAGACGT CTCAGGGCGC AGGTGCCTTG GGCCGGGATT AGTAGCCGTC 300

TGAACTGGAG TGGAGTAGGA GAAAGAGGAA GCGTCTTGGG CTGGGTCTGC TTGAGCAACT 360

GGTGAAACTC CGCGCCTCAC GCCCCGGGTG TGTCCTTGTC CAGGGGCGAC GAGCATTCTG 420

GGCGAAGTCC GCACGCCTCT TGTTCGAGGC GGAAGACGGG GTCTTGATGC TTTCTCCTTG 480

GGTCGGGGAC TGTCTCGAGG CATGCATGTC CAGTGACTCT TGTGTTTGGT GNTGCTTCCC 540

TCTCAGATCT TCTCACCGNG GTGGGCAACT CTGTTTAGGC ATATTATCCA TAGNGGAGGC 600

TGGATGGTTG AAANAATTGA GGTNATTTTC CATAATCAAG TGAAATTTGA TAGAGTCCGN 660

CTTTNGGGGT GNAAGGGTTA AAAAAAAATA ACGGAAATGG AACAATGAGG TCAAGGATTA 720

GTTGAGTTGN TAGNGGTTCA ATTAGANATG AAGGNATCTA AAATAGGAGT AGAGAANNNG 780

TTNAAAGAGG GAAAATTTTG CC 802

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 793 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

ATATGCAGCC GCGTAATTAA CCTCACTAAA GGGAACAAAA GCTGGGTACC GGGCCCCCCC 60

TCGAGGTCGA CGGTATCGAT AAGCTTGATA TCGAATTCCT GCAGCCCGGG GGATCCGCCC 120

CGCGGCCTCC CAAAGTGCTG GGATTACAGG CGTGAGCCAC CGCCCCGGGN CTCACATTTT 180

ATTTCTATTG GCTAGCGCTG CTCTAAATCT TCTGTTCCTT CTGCTACACC AGGCCTAACA 240

CTCAAAATCC CTGCCAACCT TTTCCTTCCT GAAGCTTCCC TCCCCTTCCT CAGCTCTGGC 300

GACCCTGCGC TGTGGTGGTT CTCCAACCAC ACTCATTCTC CTCAGCTGGC TCCTTGCTCT 360

TCTTCCACCC CCTCGNTGGA AGTGTTCCTA AGTGTTTGGC TTGGCCTCCT CTTCCCCTTC 420

CTTAGCTTAG ACTTCTCCAC TGCTCCAACA TCAACTGGAA ATCTATGGAA TTGATTCCTG 480

TTTCAGCTCC AGTCCTGTTC ACAGGGGATT TTCANCTGGT GGCATTTCCA AAGTGAAATT 540

CCAAACCACT TCCTCGGCCT CCTCTTCTAA ANCAGGTCTT TCTTCCTAAC TTCCTTATTC 600

TTGAGAATGT CTCTGCATGT TCTTAAANTG AAAACTCCTA GTCAAATTCA AATTTATCCC 660

TGATCCCAAA TGGTCCCATT CCCGTAGGGT TTNTGTAGCC TGCACACCGA GGTCGGANTT 720

TATNNATTCA CCGATTATGG AAAGTAACCA ATCTTNACCA NCCAGCTCAT TTGTTNTNTG 780

CTAAGAGGGT NCC 793

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 440 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

AAAGTCATGG ATTCCTTTAG GTAGCTACAT TATCAACCTT TTTGAGAATA AAATGAATTG 60

AGAGTGTTAC AGTCTAATTC TATATCACAT GTAACTTTTA TTTGGATATA TCAGTAATAG 120

TGCTTTTTCN TTTTTTTTTT TTNTTTTTTT TNNTTTTNGG GGANAGAGTC TCGCTCTGTC 180

GCCAGGTTGG AGTGCAATGG TGCGATCTTG GCTCACTGAA AGCTCCACCN CCCGGGTTCA 240

AGTGATTCTC CTGCCTCAGC CNCCCAAGTA GNTGGGACTA CAGGGGTGCG CCACCACGCC 300

TGGGATAATT TTGGGNTTTT TAGTAGAGAT GGCGTTTCAC CANCTTGGNG CAGGCTGGTC 360

TTGGAACTCC TGANATCATG ATCTGCCTGC CTTAGCCTCC CCAAAGTGCT GGGATTNCAG 420

GGGTGAGCCA CTGTTCCTGG 440

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 453 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

CTTAGTCTGT NTCGTAGTCA TATTAATTGT AAGTNTACAC TAATAAGAAT GTGTCAGAGC 60

TCTTAATGTC AAAACTTTGA TTACACAGTC CCTTTAAGGC AGTTCTGTTT TAACCCCAGG 120

TGGGTTAAAT ATTCCAGCTA TCTGAGGAGC TTTTNGATAA TTGGACCTCA CCTTAGTAGT 180

TCTCTACCCT GGCCACACAT TAGAATCACT TGGGAGCTTT TAAAACTGTA AGCTCTGCCC 240

TGAGATATTC TTACTCAATT TAATTGTGTA GTTTTTAAAA TTCCCCAGGA AATTCTGGTA 300

TTTCTGTTTA GGAACCGCTG CCTCAAGCCT AGCAGNACAG ATATGTAGGA AATTAGCTCT 360

GTAAGGTTGG TCTTACAGGG GATAAACAGA TCCTTCCTTA GNCCCTGGGA CTTAATCACT 420

GAGAGTTTGG GTGGNGGTTT NGNATTTAAT GAC 453

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 369 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

GACACACATT CACACATAAT TATGAAAGCA TTTTCAGGCA AAACTCAATC ACAAGTCTGG 60

GTTTTTAACA TAGTTAACTG AATATTTCCC TTGGGGGGTT AAATTTTAGA ACAGACGTNC 120

ATNCAATCTG GAAGAAGAGC TATGAAAAAA ACCTAGCTTG GGTNGGTTTC ATAGGGTNCA 180

TTATGNACAC ATTGTTATTT TATCCCTTAA TNCTAGTAAA GAAATAGAAT CTGAAAATAA 240

GTAAAACTAC TTGGAAAAAA NTTAAAAGAT ACAGAAATTT CTATCTTAAA TGATGTGTGG 300

GCCNCTGTGA TTTTAGTNGG GNTGGTTAAA ANCCCAGAGG TGAAGAGNAT NCTCTATGCT 360

GTGNGGGGG 369

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 516 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

GCTCATCATG CTTCACGGGG GAGGCTGTGC GGGAAGAATG CTCCCACACA GNATAAAGAA 60

TGCTCCCGCA CAGGATAGAG AATGCCCCCG CACAGCATAG AGAAGCCCCC GCACAGCATA 120

GAGAATGCCC CCNCACAGCA TAGAGAAGCC CCCGCACAGC ATAGAGAATG CTCTTCACCT 180

CTGGGTTTTT AACCAGCCAA ACTAAAATCA CAGAGGSCMA CACATCATTT AAGATAGAAA 240

TTTCTGTATC TTTTAATTTY TTTCMAAGTA GTTTTACTTA TTTTCAGATT CTATTTCTTT 300

ACTAGAATTA AGGGATAAAA TAACAATGTG TGCATAATGA ACCCTATGAA ACMAACMMAA 360

GCTAGGTTTT TTTCATAGST CTTCTTCCAG ATTGAATGAA CGTCTGTTCT AAAATTTAAC 420

CCCCCAGGGA AATATTCAGT TAACTATGTT AAAAACCCAG ACTTGTGATT GAGTTTTGCC 480

TGAAAATGCT TTCATAATTA TGTGTGAATG TGTGTC 516

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 121 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

GTATAATGCA GGTGCTATAA GGTGAGCATG AGACACAGAT CTTTGCTTTC CACCCTGTTC 60

TTCTTATGGT TGGGTATTCT TGTCACAGTA ACTTAACTGA TCTAGGAAAG AAAAAATGTT 120

T 121

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

TGGAGACTGG AACACAAC 18

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

GTGTGGCCAG GGTAGAGAAC T 21

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

ATCTCCGGCA GGCATATCT 19

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

TGAAATCACA GCCAAGATGA G 21

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

CCATAGCCTG TTTCGTAGC 19

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

CCATAGCCTA TTTCGTAGC 19

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2791 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

TGGGACAGGC AGCTCCGGGG TCCGCGGTTT CACATCGGAA ACAAAACAGC GGCTGGTCTG 60

GAAGGAACCT GAGCTACGAG CCGCGGCGGC AGCGGGGCGG CGGGGAAGCG TATACCTAAT 120

CTGGGAGCCT GCAAGTGACA ACAGCCTTTG CGGTCCTTAG ACAGCTTGGC CTGGAGGAGA 180

ACACATGAAA GAAAGAACCT CAAGAGGCTT TGTTTTCTGT GAAACAGTAT TTCTATACAG 240

TTGCTCCAAT GACAGAGTTA CCTGCACCGT TGTCCTACTT CCAGAATGCA CAGATGTCTG 300

AGGACAACCA CCTGAGCAAT ACTGTACGTA GCCAGAATGA CAATAGAGAA CGGCAGGAGC 360

ACAACGACAG ACGGAGCCTT GGCCACCCTG AGCCATTATC TAATGGACGA CCCCAGGGTA 420

ACTCCCGGCA GGTGGTGGAG CAAGATGAGG AAGAAGATGA GGAGCTGACA TTGAAATATG 480

GCGCCAAGCA TGTGATCATG CTCTTTGTCC CTGTGACTCT CTGCATGGTG GTGGTCGTGG 540

CTACCATTAA GTCAGTCAGC TTTTATACCC GGAAGGATGG GCAGCTAATC TATACCCCAT 600

TCACAGAAGA TACCGAGACT GTGGGCCAGA GAGCCCTGCA CTCAATTCTG AATGCTGCCA 660

TCATGATCAG TGTCATTGTT GTCATGACTA TCCTCCTGGT GGTTCTGTAT AAATACAGGT 720

GCTATAAGGT CATCCATGCC TGGCTTATTA TATCATCTCT ATTGTTGCTG TTCTTTTTTT 780

CATTCATTTA CTTGGGGGAA GTGTTTAAAA CCTATAACGT TGCTGTGGAC TACATTACTG 840

TTGCACTCCT GATCTGGAAT TTTGGTGTGG TGGGAATGAT TTCCATTCAC TGGAAAGGTC 900

CACTTCGACT CCAGCAGGCA TATCTCATTA TGATTAGTGC CCTCATGGCC CTGGTGTTTA 960

TCAAGTACCT CCCTGAATGG ACTGCGTGGC TCATCTTGGC TGTGATTTCA GTATATGATT 1020

TAGTGGCTGT TTTGTGTCCG AAAGGTCCAC TTCGTATGCT GGTTGAAACA GCTCAGGAGA 1080

GAAATGAAAC GCTTTTTCCA GCTCTCATTT ACTCCTCAAC AATGGTGTGG TTGGTGAATA 1140

TGGCAGAAGG AGACCCGGAA GCTCAAAGGA GAGTATCCAA AAATTCCAAG TATAATGCAG 1200

AAAGCACAGA AAGGGAGTCA CAAGACACTG TTGCAGAGAA TGATGATGGC GGGTTCAGTG 1260

AGGAATGGGA AGCCCAGAGG GACAGTCATC TAGGGCCTCA TCGCTCTACA CCTGAGTCAC 1320

GAGCTGCTGT CCAGGAACTT TCCAGCAGTA TCCTCGCTGG TGAAGACCCA GAGGAAAGGG 1380

GAGTAAAACT TGGATTGGGA GATTTCATTT TCTACAGTGT TCTGGTTGGT AAAGCCTCAG 1440

CAACAGCCAG TGGAGACTGG AACACAACCA TAGCCTGTTT CGTAGCCATA TTAATTGGTT 1500

TGTGCCTTAC ATTATTACTC CTTGCCATTT TCAAGAAAGC ATTGCCAGCT CTTCCAATCT 1560

CCATCACCTT TGGGCTTGTT TTCTACTTTG CCACAGATTA TCTTGTACAG CCTTTTATGG 1620

ACCAATTAGC ATTCCATCAA TTTTATATCT AGCATATTTG CGGTTAGAAT CCCATGGATG 1680

TTTCTTCTTT GACTATAACC AAATCTGGGG AGGACAAAGG TGATTTTCCT GTGTCCACAT 1740

CTAACAAAGT CAAGATTCCC GGCTGGACTT TTGCAGCTTC CTTCCAAGTC TTCCTGACCA 1800

CCTTGCACTA TTGGACTTTG GAAGGAGGTG CCTATAGAAA ACGATTTTGA ACATACTTCA 1860

TCGCAGTGGA CTGTGTCCCT CGGTGCAGAA ACTACCAGAT TTGAGGGACG AGGTCAAGGA 1920

GATATGATAG GCCCGGAAGT TGCTGTGCCC CATCAGCAGC TTGACGCGTG GTCACAGGAC 1980

GATTTCACTG ACACTGCGAA CTCTCAGGAC TACCGGTTAC CAAGAGGTTA GGTGAAGTGG 2040

TTTAAACCAA ACGGAACTCT TCATCTTAAA CTACACGTTG AAAATCAACC CAATAATTCT 2100

GTATTAACTG AATTCTGAAC TTTTCAGGAG GTACTGTGAG GAAGAGCAGG CACCAGCAGC 2160

AGAATGGGGA ATGGAGAGGT GGGCAGGGGT TCCAGCTTCC CTTTGATTTT TTGCTGCAGA 2220

CTCATCCTTT TTAAATGAGA CTTGTTTTCC CCTCTCTTTG AGTCAAGTCA AATATGTAGA 2280

TTGCCTTTGG CAATTCTTCT TCTCAAGCAC TGACACTCAT TACCGTCTGT GATTGCCATT 2340

TCTTCCCAAG GCCAGTCTGA ACCTGAGGTT GCTTTATCCT AAAAGTTTTA ACCTCAGGTT 2400

CCAAATTCAG TAAATTTTGG AAACAGTACA GCTATTTCTC ATCAATTCTC TATCATGTTG 2460

AAGTCAAATT TGGATTTTCC ACCAAATTCT GAATTTGTAG ACATACTTGT ACGCTCACTT 2520

GCCCCCAGAT GCCTCCTCTG TCCTCATTCT TCTCTCCCAC ACAAGCAGTC TTTTTCTACA 2580

GCCAGTAAGG CAGCTCTGTC TGGTAGCAGA TGGTCCCATT ATTCTAGGGT CTTACTCTTT 2640

GTATGATGAA AAGAATGTGT TATGAATCGG TGCTGTCAGC CCTGCTGTCA GACCTTCTTC 2700

CACAGCAAAT GAGATGTATG CCCAAAGCGG TAGAATTAAA GAAGAGTAAA ATGGCTGTTG 2760

AAGCAAAAAA AAAAAAAAAA AAAAAAAAAA A 2791

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 467 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

Met Thr Glu Leu Pro Ala Pro Leu Ser Tyr Phe Gln Asn Ala Gln Met
1 5 10 15

Ser Glu Asp Asn His Leu Ser Asn Thr Val Arg Ser Gln Asn Asp Asn
20 25 30

Arg Glu Arg Gln Glu His Asn Asp Arg Arg Ser Leu Gly His Pro Glu
35 40 45

Pro Leu Ser Asn Gly Arg Pro Gln Gly Asn Ser Arg Gln Val Val Glu
50 55 60

Gln Asp Glu Glu Glu Asp Glu Glu Leu Thr Leu Lys Tyr Gly Ala Lys
65 70 75 80

His Val Ile Met Leu Phe Val Pro Val Thr Leu Cys Met Val Val Val
85 90 95

Val Ala Thr Ile Lys Ser Val Ser Phe Tyr Thr Arg Lys Asp Gly Gln
100 105 110

```
Leu Ile Tyr Thr Pro Phe Thr Glu Asp Thr Glu Thr Val Gly Gln Arg
        115                 120                 125

Ala Leu His Ser Ile Leu Asn Ala Ala Ile Met Ile Ser Val Ile Val
    130                 135                 140

Val Met Thr Ile Leu Leu Val Val Leu Tyr Lys Tyr Arg Cys Tyr Lys
145                 150                 155                 160

Val Ile His Ala Trp Leu Ile Ile Ser Ser Leu Leu Leu Leu Phe Phe
                165                 170                 175

Phe Ser Phe Ile Tyr Leu Gly Glu Val Phe Lys Thr Tyr Asn Val Ala
            180                 185                 190

Val Asp Tyr Ile Thr Val Ala Leu Leu Ile Trp Asn Phe Gly Val Val
        195                 200                 205

Gly Met Ile Ser Ile His Trp Lys Gly Pro Leu Arg Leu Gln Gln Ala
    210                 215                 220

Tyr Leu Ile Met Ile Ser Ala Leu Met Ala Leu Val Phe Ile Lys Tyr
225                 230                 235                 240

Leu Pro Glu Trp Thr Ala Trp Leu Ile Leu Ala Val Ile Ser Val Tyr
                245                 250                 255

Asp Leu Val Ala Val Leu Cys Pro Lys Gly Pro Leu Arg Met Leu Val
            260                 265                 270

Glu Thr Ala Gln Glu Arg Asn Glu Thr Leu Phe Pro Ala Leu Ile Tyr
        275                 280                 285

Ser Ser Thr Met Val Trp Leu Val Asn Met Ala Glu Gly Asp Pro Glu
    290                 295                 300

Ala Gln Arg Arg Val Ser Lys Asn Ser Lys Tyr Asn Ala Glu Ser Thr
305                 310                 315                 320

Glu Arg Glu Ser Gln Asp Thr Val Ala Glu Asn Asp Asp Gly Gly Phe
                325                 330                 335

Ser Glu Glu Trp Glu Ala Gln Arg Asp Ser His Leu Gly Pro His Arg
            340                 345                 350

Ser Thr Pro Glu Ser Arg Ala Ala Val Gln Glu Leu Ser Ser Ser Ile
        355                 360                 365

Leu Ala Gly Glu Asp Pro Glu Glu Arg Gly Val Lys Leu Gly Leu Gly
    370                 375                 380

Asp Phe Ile Phe Tyr Ser Val Leu Val Gly Lys Ala Ser Ala Thr Ala
385                 390                 395                 400

Ser Gly Asp Trp Asn Thr Thr Ile Ala Cys Phe Val Ala Ile Leu Ile
                405                 410                 415
```

Gly Leu Cys Leu Thr Leu Leu Leu Ala Ile Phe Lys Lys Ala Leu
420 425 430

Pro Ala Leu Pro Ile Ser Ile Thr Phe Gly Leu Val Phe Tyr Phe Ala
435 440 445

Thr Asp Tyr Leu Val Gln Pro Phe Met Asp Gln Leu Ala Phe His Gln
450 455 460

Phe Tyr Ile
465

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1962 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

ACCANACANC GGCAGCTGAG GCGGAAACCT AGGCTGCGAG CCGGCCGCCC GGGCGCGGAG 60

AGAGAAGGAA CCAACACAAG ACAGCAGCCC TTCGAGGTCT TTAGGCAGCT TGGAGGAGAA 120

CACATGAGAG AAAGAATCCC AAGAGGTTTT GTTTTCTTTG AGAAGGTATT TCTGTCCAGC 180

TGCTCCAATG ACAGAGATAC CTGCACCTTT GTCCTACTTC CAGAATGCCC AGATGTCTGA 240

GGACAGCCAC TCCAGCAGCG CCATCCGGAG CCAGAATGAC AGCCAAGAAC GGCAGCAGCA 300

GCATGACAGG CAGAGACTTG ACAACCCTGA GCCAATATCT AATGGGCGGC CCCAGAGTAA 360

CTCAAGACAG GTGGTGGAAC AAGATGAGGA GGAAGACGAA GAGCTGACAT TGAAATATGG 420

AGCCAAGCAT GTCATCATGC TCTTTGTCCC CGTGACCCTC TGCATGGTCG TCGTCGTGGC 480

CACCATCAAA TCAGTCAGCT TCTATACCCG GAAGGACGGT CAGCTAATCT ACACCCCATT 540

CACAGAAGAC ACTGAGACTG TAGGCCAAAG AGCCCTGCAC TCGATCCTGA ATGCGGCCAT 600

CATGATCAGT GTCATTGTCA TTATGACCAT CCTCCTGGTG GTCCTGTATA AATACAGGTG 660

CTACAAGGTC ATCCACGCCT GGCTTATTAT TTCATCTCTG TTGTTGCTGT TCTTTTTTTC 720

GTTCATTTAC TTAGGGGAAG TATTTAAGAC CTACAATGTC GCCGTGGACT ACGTTACAGT 780

AGCACTCCTA ATCTGGAATT TTGGTGTGGT CGGGATGATT GCCATCCACT GGAAAGGCCC 840

CCTTCGACTG CAGCAGGCGT ATCTCATTAT GATCAGTGCC CTCATGGCCC TGGTATTTAT 900

CAAGTACCTC CCCGAATGGA CCGCATGGCT CATCTTGGCT GTGATTTCAG TATATGATTT 960

GGTGGCTGTT TTATGTCCCA AAGGCCCACT TCGTATGCTG GTTGAAACAG CTCAGGAAAG 1020

AAATGAGACT CTCTTTCCAG CTCTTATCTA TTCCTCAACA ATGGTGTGGT TGGTGAATAT 1080

GGCTGAAGGA GACCCAGAAG CCCAAAGGAG GGTACCCAAG AACCCCAAGT ATAACACACA 1140

AAGAGCGGAG AGAGAGACAC AGGACAGTGG TTCTGGGAAC GATGATGGTG GCTTCAGTGA 1200

GGAGTGGGAG GCCCAAAGAG ACAGTCACCT GGGGCCTCAT CGCTCCACTC CCGAGTCAAG 1260

AGCTGCTGTC CAGGAACTTT CTGGGAGCAT TCTAACGAGT GAAGACCCGG AGGAAAGAGG 1320

AGTAAAACTT GGACTGGGAG ATTTCATTTT CTACAGTGTT CTGGTTGGTA AGGCCTCAGC 1380

AACCGCCAGT GGAGACTGGA ACACAACCAT AGCCTGCTTT GTAGCCATAC TGATCGGCCT 1440

GTGCCTTACA TTACTCCTGC TCGCCATTTT CAAGAAAGCG TTGCCAGCCC TCCCCATCTC 1500

CATCACCTTC GGGCTCGTGT TCTACTTCGC CACGGATTAC CTTGTGCAGC CCTTCATGGA 1560

CCAACTTGCA TTCCATCAGT TTTATATCTA GCCTTTCTGC AGTTAGAACA TGGATGTTTC 1620

TTCTTTGATT ATCAAAAACA CAAAAACAGA GAGCAAGCCC GAGGAGGAGA CTGGTGACTT 1680

TCCTGTGTCC TCAGCTAACA AAGGCAGGAC TCCAGCTGGA CTTCTGCAGC TTCCTTCCGA 1740

GTCTCCCTAG CCACCCGCAC TACTGGACTG TGGAAGGAAG CGTCTACAGA GGAACGGTTT 1800

CCAACATCCA TCGCTGCAGC AGACGGTGTC CCTCAGTGAC TTGAGAGACA AGGACAAGGA 1860

AATGTGCTGG GCCAAGGAGC TGCCGTGCTC TGCTAGCTTT GACCGTGGGC ATGGAGATTT 1920

ACCCGCACTG TGAACTCTCT AAGGTAAACA AAGTGAGGTG AACC 1964

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2285 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

GAATTCGGCA CGAGGGCATT TCCAGCAGTG AGGAGACAGC CAGAAGCAAG CTTTTGGAGC 60

TGAAGGAACC TGAGACAGAA GCTAGTCCCC CCTCTGAATT TTACTGATGA AGAAACTGAG 120

GCCACAGAGC TAAAGTGACT TTTCCCAAGG TCGCCCAGCG AGGACGTGGG ACTTCTCAGA 180

CGTCAGGAGA GTGATGTGAG GGAGCTGTGT GACCATAGAA AGTGACGTGT TAAAAACCAG 240

CGCTGCCCTC TTTGAAAGCC AGGGAGCATC ATTCATTTAG CCTGCTGAGA AGAAGAAACC 300

AAGTGTCCGG GATTCAAGAC CTCTCTGCGG CCCCAAGTGT TCGTGGTGCT TCCAGAGGCA 360

GGGCTATGCT CACATTCATG GCCTCTGACA GCGAGGAAGA AGTGTGTGAT GAGCGGACGT 420

CCCTAATGTC GGCCGAGAGC CCCACGCCGC GCTCCTGCCA GGAGGGCAGG CAGGGCCCAG 480

AGGATGGAGA GAATACTGCC CAGTGGAGAA GCCAGGAGAA CGAGGAGGAC GGTGAGGAGG 540

ACCCTGACCG CTATGTCTGT AGTGGGGTTC CCGGGCGGCC GCCAGGCCTG GAGGAAGAGC 600

TGACCCTCAA ATACGGAGCG AAGCATGTGA TCATGCTGTT TGTGCCTGTC ACTCTGTGCA 660

TGATCGTGGT GGTAGCCACC ATCAAGTCTG TGCGCTTCTA CACAGAGAAG AATGGACAGC 720

TCATCTACAC GCCATTCACT GAGGACACAC CCTCGGTGGG CCAGCGCCTC CTCAACTCCG 780

TGCTGAACAC CCTCATCATG ATCAGCGTCA TCGTGGTTAT GACCATCTTC TTGGTGGTGC 840

TCTACAAGTA CCGCTGCTAC AAGTTCATCC ATGGCTGGTT GATCATGTCT TCACTGATGC 900

TGCTGTTCCT CTTCACCTAT ATCTACCTTG GGGAAGTGCT CAAGACCTAC AATGTGGCCA 960

TGGACTACCC CACCCTCTTG CTGACTGTCT GGAACTTCGG GGCAGTGGGC ATGGTGTGCA 1020

TCCACTGGAA GGGCCCTCTG GTGCTGCAGC AGGCCTACCT CATCATGATC AGTGCGCTCA 1080

TGGCCCTAGT GTTCATCAAG TACCTCCCAG AGTGGTCCGC GTGGGTCATC CTGGGCGCCA 1140

TCTCTGTGTA TGATCTCGTG GCTGTGCTGT GTCCCAAAGG GCCTCTGAGA ATGCTGGTAG 1200

AAACTGCCCA GGAGAGAAAT GAGCCCATAT TCCCTGCCCT GATATACTCA TCTGCCATGG 1260

TGTGGACGGT TGGCATGGCG AAGCTGGACC CCTCCTCTCA GGGTGCCCTC CAGCTCCCCT 1320

ACGACCCGGA GATGGAAGAA GACTCCTATG ACAGTTTTGG GGAGCCTTCA TACCCCGAAG 1380

TCTTTGAGCC TCCCTTGACT GGCTACCCAG GGGAGGAGCT GGAGGAAGAG GAGGAAAGGG 1440

GCGTGAAGCT TGGCCTCGGG GACTTCATCT TCTACAGTGT GCTGGTGGGC AAGGCGGCTG 1500

CCACGGGCAG CGGGGACTGG AATACCACGC TGGCCTGCTT CGTGGCCATC CTCATTGGCT 1560

TGTGTCTGAC CCTCCTGCTG CTTGCTGTGT TCAAGAAGGC GCTGCCCGCC CTCCCCATCT 1620

CCATCACGTT CGGGCTCATC TTTTACTTCT CCACGGACAA CCTGGTGCGG CCGTTCATGG 1680

ACACCCTGGC CTCCCATCAG CTCTACATCT GAGGGACATG GTGTGCCACA GGCTGCAAGC 1740

TGCAGGGAAT TTTCATTGGA TGCAGTTGTA TAGTTTTACA CTCTAGTGCC ATATATTTTT 1800

AAGACTTTTC TTTCCTTAAA AAATAAAGTA CGTGTTTACT TGGTGAGGAG GAGGCAGAAC 1860

CAGCTCTTTG GTGCCAGCTG TTTCATCACC AGACTTTGGC TCCCGCTTTG GGGAGCGCCT 1920

CGCTTCACGG ACAGGAAGCA CAGCAGGTTT ATCCAGATGA ACTGAGAAGG TCAGATTAGG 1980

GTGGGGAGAA GAGCATCCGG CATGAGGGCT GAGATGCCCA AAGAGTGTGC TCGGGAGTGG 2040

CCCCTGGCAC CTGGGTGCTC TGGCTGGAGA GGAAAAGCCA GTTCCCTACG AGGAGTGTTC 2100

CCAATGCTTT GTCCATGATG TCCTTGTTAT TTTATTNCCY TTANAAACTG ANTCCTNTTN 2160

TTNTTDCGGC AGTCACMCTN CTGGGRAGTG GCTTAATAGT AANATCAATA AANAGNTGAG 2220

TCCTNTTAGA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 2280

AAAAA 2285

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 448 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

Met Leu Thr Phe Met Ala Ser Asp Ser Glu Glu Glu Val Cys Asp Glu
1 5 10 15

Arg Thr Ser Leu Met Ser Ala Glu Ser Pro Thr Pro Arg Ser Cys Gln
20 25 30

Glu Gly Arg Gln Gly Pro Glu Asp Gly Glu Asn Thr Ala Gln Trp Arg
35 40 45

Ser Gln Glu Asn Glu Glu Asp Gly Glu Glu Asp Pro Asp Arg Tyr Val
50 55 60

Cys Ser Gly Val Pro Gly Arg Pro Pro Gly Leu Glu Glu Glu Leu Thr
65 70 75 80

Leu Lys Tyr Gly Ala Lys His Val Ile Met Leu Phe Val Pro Val Thr
85 90 95

Leu Cys Met Ile Val Val Val Ala Thr Ile Lys Ser Val Arg Phe Tyr
100 105 110

Thr Glu Lys Asn Gly Gln Leu Ile Tyr Thr Pro Phe Thr Glu Asp Thr
115 120 125

Pro Ser Val Gly Gln Arg Leu Leu Asn Ser Val Leu Asn Thr Leu Ile
130 135 140

Met Ile Ser Val Ile Val Val Met Thr Ile Phe Leu Val Val Leu Tyr
145 150 155 160

Lys Tyr Arg Cys Tyr Lys Phe Ile His Gly Trp Leu Ile Met Ser Ser
165 170 175

Leu Met Leu Leu Phe Leu Phe Thr Tyr Ile Tyr Leu Gly Glu Val Leu
180 185 190

Lys Thr Tyr Asn Val Ala Met Asp Tyr Pro Thr Leu Leu Leu Thr Val
195 200 205

Trp Asn Phe Gly Ala Val Gly Met Val Cys Ile His Trp Lys Gly Pro
210 215 220

Leu Val Leu Gln Gln Ala Tyr Leu Ile Met Ile Ser Ala Leu Met Ala
225 230 235 240

Leu Val Phe Ile Lys Tyr Leu Pro Glu Trp Ser Ala Trp Val Ile Leu
245 250 255

Gly Ala Ile Ser Val Tyr Asp Leu Val Ala Val Leu Cys Pro Lys Gly
260 265 270

Pro Leu Arg Met Leu Val Glu Thr Ala Gln Glu Arg Asn Glu Pro Ile
275 280 285

Phe Pro Ala Leu Ile Tyr Ser Ser Ala Met Val Trp Thr Val Gly Met
290 295 300

Ala Lys Leu Asp Pro Ser Ser Gln Gly Ala Leu Gln Leu Pro Tyr Asp
305 310 315 320

Pro Glu Met Glu Glu Asp Ser Tyr Asp Ser Phe Gly Glu Pro Ser Tyr
325 330 335

Pro Glu Val Phe Glu Pro Pro Leu Thr Gly Tyr Pro Gly Glu Glu Leu
340 345 350

Glu Glu Glu Glu Glu Arg Gly Val Lys Leu Gly Leu Gly Asp Phe Ile
355 360 365

Phe Tyr Ser Val Leu Val Gly Lys Ala Ala Ala Thr Gly Ser Gly Asp
370 375 380

Trp Asn Thr Thr Leu Ala Cys Phe Val Ala Ile Leu Ile Gly Leu Cys
385 390 395 400

Leu Thr Leu Leu Leu Leu Ala Val Phe Lys Lys Ala Leu Pro Ala Leu
405 410 415

Pro Ile Ser Ile Thr Phe Gly Leu Ile Phe Tyr Phe Ser Thr Asp Asn
420 425 430

Leu Val Arg Pro Phe Met Asp Thr Leu Ala Ser His Gln Leu Tyr Ile
435 440 445

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 372 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

```
Glu Glu Leu Thr Leu Lys Tyr Gly Ala Lys His Val Ile Met Leu Phe
1               5                  10                  15

Val Pro Val Thr Leu Cys Met Ile Val Val Ala Thr Ile Lys Ser
            20                  25                  30

Val Arg Phe Tyr Thr Glu Lys Asn Gly Gln Leu Ile Tyr Thr Pro Phe
        35                  40                  45

Thr Glu Asp Thr Pro Ser Val Gly Gln Arg Leu Leu Asn Ser Val Leu
    50                  55                  60

Asn Thr Leu Ile Met Ile Ser Val Ile Val Val Met Thr Ile Phe Leu
65                  70                  75                  80

Val Val Leu Tyr Lys Tyr Arg Cys Tyr Lys Phe Ile His Gly Trp Leu
                85                  90                  95

Ile Met Ser Ser Leu Met Leu Leu Phe Leu Phe Thr Tyr Ile Tyr Leu
            100                 105                 110

Gly Glu Val Leu Lys Thr Tyr Asn Val Ala Met Asp Tyr Pro Thr Leu
        115                 120                 125

Leu Leu Thr Val Trp Asn Phe Gly Ala Val Gly Met Val Cys Ile His
    130                 135                 140

Trp Lys Gly Pro Leu Val Leu Gln Gln Ala Tyr Leu Ile Met Ile Ser
145                 150                 155                 160

Ala Leu Met Ala Leu Val Phe Ile Lys Tyr Leu Pro Glu Trp Ser Ala
                165                 170                 175

Trp Val Ile Leu Gly Ala Ile Ser Val Tyr Asp Leu Val Ala Val Leu
            180                 185                 190

Cys Pro Lys Gly Pro Leu Arg Met Leu Val Glu Thr Ala Gln Glu Arg
        195                 200                 205

Asn Glu Pro Ile Phe Pro Ala Leu Ile Tyr Ser Ser Ala Met Val Trp
    210                 215                 220

Thr Val Gly Met Ala Lys Leu Asp Pro Ser Ser Gln Gly Ala Leu Gln
225                 230                 235                 240

Leu Pro Tyr Asp Pro Glu Met Glu Glu Asp Ser Tyr Asp Ser Phe Gly
                245                 250                 255
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Glu Pro Ser Tyr Pro Glu Val Phe Glu Pro Pro Leu Thr Gly Tyr Pro
            260                 265                 270

Gly Glu Glu Leu Glu Glu Glu Glu Glu Arg Gly Val Lys Leu Gly Leu
        275                 280                 285

Gly Asp Phe Ile Phe Tyr Ser Val Leu Val Gly Lys Ala Ala Ala Thr
    290                 295                 300

Gly Ser Gly Asp Trp Asn Thr Thr Leu Ala Cys Phe Val Ala Ile Leu
305                 310                 315                 320

Ile Gly Leu Cys Leu Thr Leu Leu Leu Leu Ala Val Phe Lys Lys Ala
                325                 330                 335

Leu Pro Ala Leu Pro Ile Ser Ile Thr Phe Gly Leu Ile Phe Tyr Phe
            340                 345                 350

Ser Thr Asp Asn Leu Val Arg Pro Phe Met Asp Thr Leu Ala Ser His
        355                 360                 365

Gln Leu Tyr Ile
    370
```

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

GGTACCGCCA CCATGACAGA GGTACCTGCA C 31

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

GAATTCACTG GCTGTAGAAA AAGAC 25

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

GGATCCGGTC CACTTCGTAT GCTG 24

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

TTTTTTGAAT TCTTAGGCTA TGGTTGTGTT CCA 33

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

GATTAGTGGT TGTTTTGTG 19

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

GATTAGTGGC TGTTTTGTG 19

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

TTTTTCCAGC TCTCATTTA 19

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

TTTTTCCAGT TCTCATTTA 19

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

TACAGTGTTC TGGTTGGTA 19

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

TACAGTGTTC TGGTTGGTA 19

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

TACAGTGTTG TGGTTGGTA 19

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1092 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

GTCTAGATAA GNCAACATTC AGGGGTAGAA GGGGACTGTT TATTTTTTCC TTTAGTCTCT 60

CTTAAAGAGT GAGAAAAATT TTCCCAGGAA TCCCGGTGGA CTTTGCTTCA CCACTCATAG 120

GTTCATACCA AGTTACAACC CCACAACCTT AGAGCTTTTG TTAGGAAGAG GCTTGGTGGG 180

ATTACCGTGC TTGGCTTGGC TTGGTCAGGA TTCACCACCA GAGTCATGTG GGAGGGGGTG 240

GGAACCCAAA CAATTCAGGA TTCTGCCCTC AGGAAATAAA GGAGAAAATA GCTGTTGGAT 300

AAACTACCAG CAGGCACTGC TACAGCCCAT GCTTTGTGGT TTAAGGGCCA GCTAGTTACA 360

ATGACAGCTA GTTACTGTTT CCATGTAATT TTCTTAAAGG TATTAAATTT TTCTAAATAT 420

TAGAGCTGTA ACTTCCACTT TCTCTTGAAG GCACAGWAAG GGAGTCACAA GACACTGTTG 480

CAGAGAATGA TGATGGCGGG TTCAGTGAGG AATGGGAASC CCAGRGGGAC ANTCATCTAG 540

GGCCTCATCG CTCTACACCT GAGTCACGAG CTKCTNTCCA GGRACTTTCC ANCAGTATCC 600

TCGCTGGTGA AGACCCAGAG GAAAGNATGT TCANTTCTCC ATNTTTCAAA GTCATGGATT 660

CCTTTAGGTA GCTACATTAT CAACCTTTTT GAGAATAAAA TGAATTGAGA GTGTTACAGT 720

CTAATTCTAT ATCACATGTA ACTTTTATTT GGATATATCA GTAATAGTGC TTTTTYNTTT 780

TTTTTTTTTT TTTTTTTTTT TTTTNGGNGA NAGAGTCTCG CTCTGTCGCC AGGTTGGAGT 840

GCAATGGTGC GATCTTGGCT CACTGAAAGC TCCACCNCCC GGGTTCAAGT GATTCTCCTG 900

CCTCAGCCNC CCAAGTAGNT GGGACTACAG GGGTGCGCCA CCACGCCTGG GATAATTTTG 960

GGNTTTTTAG TAGAGATGGC GTTTCACCAN CTTGGNGCAG GCTGGTCTTG GAACTCCTGA 1020

NATCATGATC TGCCTGCCTT AGCCTCCCCA AAGTGCTGGG ATTNCAGGGG TGAGCCACTG 1080

TTCCTGGGCC TC 1092

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1003 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

CTGCAGTGAG CCGAGATCAT GCTGCTGTAC TCCAGCCTGG GCCACAGAGC CAAACTCCAT 60

CTCCCAAAAA AAAAAAATAT TAATTAATAT GATNAAATGA TGCCTATCTC AGAATTCTTG 120

TAAGGATTTC TTAGKACAAG TGCTGGGTAT AAACTATANA TTCRATAGAT GNCGATTATT 180

ACTTAYTATT GTTATTGATA AATAACAGCA GCATCTACAG TTAAGACTCC AGAGTCAGTC 240

ACATAGAATC TGGNACTCCT ATTGTAGNAA ACCCCNMMAG AAAGAAAACA CAGCTGAAGC 300

CTAATTTTGT ATATCATTTA CTGACTTCTC TCATTCATTG TGGGGTTGAG TAGGGCAGTG 360

ATATTTTTGA ATTGTGAAAT CATANCAAAG AGTGACCAAC TTTTTAATAT TTGTAACCTT 420

TCCTTTTTAG GGGGAGTAAA ACTTGGATTG GGAGATTTCA TTTTCTACAG TGTTCTGGTT 480

GGTAAAGCCT CAGCAACAGC CAGTGGAGAC TGGAACACAA CCATAGCCTG TTTCGTAGCC 540

ATATTAATTG TMMSTATACA CTAATAAGAA TGTGTCAGAG CTCTTAATGT CMAAACTTTG 600

ATTACACAGT CCCTTTAAGG CAGTTCTGTT TTAACCCCAG GTGGGTTAAA TATTCCAGCT 660

ATCTGAGGAG CTTTTNGATA ATTGGACCTC ACCTTAGTAG TTCTCTACCC TGGCCACACA 720

TTAGAATCAC TTGGGAGCTT TTAAAACTGT AAGCTCTGCC CTGAGATATT CTTACTCAAT 780

TTAATTGTGT AGTTTTTAAA ATTCCCCAGG AAATTCTGGT ATTTCTGTTT AGGAACCGCT 840

GCCTCAAGCC TAGCAGCACA GATATGTAGG AAATTAGCTC TGTAAGGTTG GTCTTACAGG 900

GATAAACAGA TCCTTCCTTA GTCCCTGGAC TTAATCACTG AGAGTTTGGG TGGTGGTTTT 960

GGATTTAATG ACACAACCTG TAGCATGCAG TGTTACTTAA GAC 1003

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1726 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

GGATCCCTCC CCTTTTTAGA CCATACAAGG TAACTTCCGG ACGTTGCCAT GGCATCTGTA 60

AACTGTCATG GTGTTGGCGG GGAGTGTCTT TTAGCATGCT AATGTATTAT AATTAGCGTA 120

TAGTGAGCAG TGAGGATAAC CAGAGGTCAC TCTCCTCACC ATCTTGGTTT TGGTGGGTTT 180

TGGCCAGCTT CTTTATTGCA ACCAGTTTTA TCAGCAAGAT CTTTATGAGC TGTATCTTGT 240

GCTGACTTCC TATCTCATCC CGNAACTAAG AGTACCTAAC CTCCTGCAAA TTGMAGNCCA 300

GNAGGTCTTG GNCTTATTTN ACCCAGCCCC TATTCAARAT AGAGTNGYTC TTGGNCCAAA 360

CGCCYCTGAC ACAAGGATTT TAAAGTCTTA TTAATTAAGG TAAGATAGKT CCTTGSATAT 420

GTGGTCTGAA ATCACAGAAA GCTGAATTTG GAAAAAGGTG CTTGGASCTG CAGCCAGTAA 480

ACAAGTTTTC ATGCAGGTGT CAGTATTTAA GGTACATCTC AAAGGATAAG TACAATTGTG 540

TATGTTGGGA TGAACAGAGA GAATGGAGCA ANCCAAGACC CAGGTAAAAG AGAGGACCTG 600

AATGCCTTCA GTGAACAATG ATAGATAATC TAGACTTTTA AACTGCATAC TTCCTGTACA 660

TTGTTTTTTC TTGCTTCAGG TTTTTAGAAC TCATAGTGAC GGGTCTGTTG TTAATCCCAG 720

GTCTAACCGT TACCTTGATT CTGCTGAGAA TCTGATTTAC TGAAAATGTT TTTCTTGTGC 780

TTATAGAATG ACAATAGAGA ACGGCAGGAG CACAACGACA GACGGAGCCT TGGCCACCCT 840

GANCCATTAT CTAATGGACG ACCCAGGGTA ACTCCCGGCA GGTGGTGGAN CAAGATGAGG 900

AAGAAGATGA GGANCTGACA TTGAAATATG NCGSCAAGCA TGTGATCATG CTCTTTGKCC 960

CTGTGACTCT CTGCATGGTG GTGGTCGTGG NTACCATTAA GTCAGTCAGC TTTTATACCC 1020

GGAAGGATGG GCAGCTGTAC GTATGAGTTT KGTTTTATTA TTCTCAAASC CAGTGTGGCT 1080

TTTCTTTACA GCATGTCATC ATCACCTTGA AGGCCTCTNC ATTGAAGGGG CATGACTTAG 1140

CTGGAGAGCC CATCCTCTGT GATGGTCAGG AGCAGTTGAG AGANCGAGGG GTTATTACTT 1200

CATGTTTTAA GTGGAGAAAA GGAACACTGC AGAAGTATGT TTCCTGTATG GTATTACTGG 1260

ATAGGGCTGA AGTTATGCTG AATTGAACAC ATAAATTCTT TTCCACCTCA GGGNCATTGG 1320

GCGCCCATTG NTCTTCTGCC TAGAATATTC TTTCCTTTNC TNACTTKGGN GGATTAAATT 1380

CCTGTCATCC CCCTCCTCTT GGTGTTATAT ATAAAGTNTT GGTGCCGCAA AAGAAGTAGC 1440

ACTCGAATAT AAAATTTTCC TTTTAATTCT CAGCAAGGNA AGTTACTTCT ATATAGAAGG 1500

GTGCACCCNT ACAGATGGAA CAATGGCAAG CGCACATTTG GGACAAGGGA GGGGAAAGGG 1560

TTCTTATCCC TGACACACGT GGTCCCNGCT GNTGTGTNCT NCCCCCACTG ANTAGGGTTA 1620

GACTGGACAG GCTTAAACTA ATTCCAATTG GNTAATTTAA AGAGAATNAT GGGGTGAATG 1680

CTTTGGGAGG AGTCAAGGAA GAGNAGGTAG NAGGTAACTT GAATGA 1726

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1883 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

CNCGTATAAA AGACCAACAT TGCCANCNAC AACCACAGGC AAGATCTTCT CCTACCTTCC 60

CCCNNGGTGT AATACCAAGT ATTCNCCAAT TTGTGATAAA CTTTCATTGG AAAGTGACCA 120

CCCTCCTTGG TTAATACATT GTCTGTGCCT GCTTTCACAC TACAGTAGCA CAGTTGAGTG 180

TTTGCCCTGG AGACCATATG ACCCATAGAG CTTAAAATAT TCAGTCTGGC TTTTTACAGA 240

GATGTTTCTG ACTTTGTTAA TAGAAAATCA ACCCAACTGG TTTAAATAAT GCACATACTT 300

TCTCTCTCAT AGAGTAGTGC AGAGGTAGNC AGTCCAGATT AGTASGGTGG CTTCACGTTC 360

ATCCAAGGAC TCAATCTCCT TCTTTCTTCT TTAGCTTCTA ACCTCTAGCT TACTTCAGGG 420

TCCAGGCTGG AGCCCTASCC TTCATTTCTG ACAGTAGGAA GGAGTAGGGG AGAAAAGAAC 480

ATAGGACATG TCAGCAGAAT TCTCTCCTTA GAAGTTCCAT ACACAACACA TCTCCCTAGA 540

AGTCATTGCC CTTACTTGTT CTCATAGCCA TCCTAAATAT AAGGGAGTCA GAAGTAAAGT 600

CTKKNTGGCT GGGAATATTG GCACCTGGAA TAAAAATGTT TTTCTGTGAA TGAGAAACAA 660

GGGGAAGATG GATATGTGAC ATTATCTTAA GACAACTCCA GTTGCAATTA CTCTGCAGAT 720

GAGAGGCACT AATTATAAGC CATATTACCT TTCTTCTGAC AACCACTTGT CAGCCCNCGT 780

GGTTTCTGTG GCAGAATCTG GTTCYATAMC AAGTTCCTAA TAANCTGTAS CCNAAAAAAT 840

TTGATGAGGT ATTATAATTA TTTCAATATA AAGCACCCAC TAGATGGAGC CAGTGTCTGC 900

TTCACATGTT AAGTCCTTCT TTCCATATGT TAGACATTTT CTTTGAAGCA ATTTTAGAGT 960

GTAGCTGTTT TTCTCAGGTT AAAAATTCTT AGCTAGGATT GGTGAGTTGG GGAAAAGTGA 1020

CTTATAAGAT NCGAATTGAA TTAAGAAAAA GAAAATTCTG TGTTGGAGGT GGTAATGTGG 1080

KTGGTGATCT YCATTAACAC TGANCTAGGG CTTTKGKGTT TGKTTTATTG TAGAATCTAT 1140

ACCCCATTCA NAGAAGATAC CGAGACTGTG GGCCAGAGAG CCCTGCACTC AATTCTGAAT 1200

GCTGCCATCA TGATCAGNGT CATTGTWGTC ATGACTANNC TCCTGGTGGT TCWGTATAAA 1260

TACAGGTGCT ATAAGGTGAG CATGAGACAC AGATCTTTGN TTTCCACCCT GTTCTTCTTA 1320

TGGTTGGGTA TTCTTGTCAC AGTAACTTAA CTGATCTAGG AAAGAAAAAA TGTTTTGTCT 1380

TCTAGAGATA AGTTAATTTT TAGTTTTCTT CCTCCTCACT GTGGAACATT CAAAAAATAC 1440

AAAAAGGAAG CCAGGTGCAT GTGTAATGCC AGGCTCAGAG GCTGAGGCAG GAGGATCGCT 1500

TGGGCCCAGG AGTTCACAAG CAGCTTGGGC AACGTAGCAA GACCCTGCCT CTATTAAAGA 1560

AAACAAAAAA CAAATATTGG AAGTATTTTA TATGCATGGA ATCTATATGT CATGAAAAAA 1620

TTAGTGTAAA ATATATATAT TATGATTAGN TATCAAGATT TAGTGATAAT TTATGTTATT 1680

TTGGGATTTC AATGCCTTTT TAGGCCATTG TCTCAAMAAA TAAAAGCAGA AAACAAAAAA 1740

AGTTGTAACT GAAAAATAAA CATTTCCATA TAATAGCACA ATCTAAGTGG GTTTTTGNTT 1800

GTTTGTTTGN TTGTTGAAGC AGGGCCTTGC CCTNYCACCC AGGNTGGAGT GAAGTGCAGT 1860

GGCACGATTT TGGCTCACTG CAG 1883

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1990 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

ATGTTTGACA ATTTCTCCGT TCCACCCTTG ATTAAATAAG GTAGTATTCA TTTTTTAAGT 60

TTTAGCTTTT GGATATATGT GTAAGTGTGG TATGCTGTCT AATGAATTAA GACAATTGGT 120

NCTKTCTTTA CCCMACANCT GGACMAAGAG CAGGCAAGAT NCAANAATCA AGTGACCCAG 180

NCAAACCAGA CACATTTTCT GCTCTCAGCT AGCTTGCCAC CTAGAAAGAC TGGTTGTCNA 240

AGTTGGAGTC CAAGAATCGC GGAGGATGTT TAAAATGCAG TTTCTCAGGT TCTCNCCACC 300

CACCAGAAGT TTTGATTCAT TGAGTGGTGG GAGAGGGCAG AGATATTTGC GATTTTAACA 360

GCATTCTCTT GATTGTGATG CAGCTGGTTC SCAAATAGGT ACCCTAAAGA AATGACAGGT 420

GTTAAATTTA GGATGGCCAT CGCTTGTATG CCGGGAGAAG CACACGCTGG GCCCAATTTA 480

TATAGGGGCT TTCGTCCTCA GCTCGAGCAR CCTCAGAACC CCGACAACCY ACGCCAGCKC 540

TCTGGGCGGA TTCCRTCAGK TGGGGAAGSC CAGGTGGAGC TCTGGKTTCT CCCCGCAATC 600

GTTTCTCCAG GCCGGAGGCC CCGCCCCCTT CCTCCTGGCT CCTCCCCTCC TCCGTGGGCC 660

GNCCGCCAAC GACGCCAGAG CCGGAAATGA CGACAACGGT GAGGGTTCTC GGGCGGGGCC 720

TGGGACAGGC AGCTCCGGGG TCCNCGNNWT NACATCGGAA ACAAAACAGC GGCTGGTCTG 780

GAAGGAACCT GAKCTACGAC CCGCGGCGGC AGCGGGGCGG CGGGGAAGCG TATGTGCGTG 840

ATGGGGAGTC CGGGCAAGCC AGGAAGGCAC CGCGGACATG GGCGGCCGCG GGCAGGGNCC 900

GGNCCTTTGT GGCCGCCCGG GCCGCGAAGC CGGTGTCCTA AAAGATGAGG GGCGGGGCGC 960

GGCCGGTTGG GGCTGGGGAA CCCCGTGTGG GAAACCAGGA GGGGCGGCCC GTTTCTCGGG 1020

CTTCGGGCGC GGCCGGGTGG AGAGAGATTC CGGGGAGCCT TGGTCCGGAA ATGCTGTTTG 1080

CTCGAAGACG TCTCAGGGCG CAGGTGCCTT GGGCCGGGAT TAGTAGCCGT CTGAACTGGA 1140

GTGGAGTAGG AGAAAGAGGA AGCGTCTTGG GCTGGGTCTG CTTGAGCAAC TGGTGAAACT 1200

CCGCGCCTCA CGCCCCGGGT GTGTCCTTGT CCAGGGGCGA CGAGCATTCT GGGCGAAGTC 1260

CGCACGCCTC TTGTTCGAGG CGGAAGACGG GGTCTTGATG CTTTCTCCTT GGTCGGGACT 1320

GTCTCGAGGC ATGCATGTCC AGTGACTCTT GTGTTTGCTG CTGCTTCCCT CTCAGATTCT 1380

TCTCACCGTT GTGGTCAGCT CTGCTTTAGG CATATTAATC CATAGTGGAG GCTGGGATGG 1440

GTGAGAGAAT TGAGGTGACT TTTCCATAAT TCAGGTGAGA TGTGATTAGA GTYCGGATCC 1500

TNCGGTGGTG GCAGAGGCTT ACCAAGAAAC ACTAACGGGA CATGGGAACC AATTGAGGAT 1560

CCAGGGAATA AAGTGTGAAG TTGACTAGGA GGTTTTCAGT TTAAGAACAT GGCAGAGACA 1620

TTCTCAGAAA TAAGGAAGTT AGGAAGAAAG ACCTGGTTTA GAGAGGAGGG CGAGGAAGTG 1680

GTTTGGAAGT GTCACTTTGG AAGTGCCAGC AGGTGAAAAT GCCCTGTGAA CAGGACTGGA 1740

GCTGAAAACA GGAATCAATT CCATAGATTT CCAGTTGATG TTGGAGCAGT GGAGAAGTCT 1800

AANCTAAGGA AGGGGAAGAG GAGGCCAAGC CAAACACTTA GGAACACTTN CNACGAGGGG 1860

GTGGAAGAAG AGCAAGGAGC CAGCTGAGGA GAATGAGTGT GGTTGGAGAA CCACCACAGC 1920

NCAGGGTCGC CAGANCTGAG GAAGGGGAGG GAAGCTTATC GAGKAMSGWC RACMKCGAGT 1980

TGGCAGGGAT 1990

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 736 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

GTCTTTCCCA TCTTCTCCAC AGAGTTTGTG CCTTACATTA TTACTCCTTG CCATTTTCAA 60

GAAAGCATTG TCAGCTCTTC CAATCTCCAT CACCTTTGGG CTTGTTTTCT ACTTTGCCAC 120

AGATTATCTT GTACAGCCTT TTATGGACCA ATTAGCATTC CATCAATTTT ATATCTAGCA 180

TATTTGCGGT TAGAATCCCA TGGATGTTTC TTCTTTGACT ATAACAAAAT CTGGGGAGGA 240

CAAAGGTGAT TTCCTGTGTC CACATCTAAC AAATCAAGAT CCCCGGCTGG ACTTTTGGAG 300

GTTCCTTCCA AGTCTTCCTG ACCACCTTGC ACTATTGGAC TTTGGAAGGA GGTGCCTATA 360

GAAAACGATT TTGAACATAC TTCATCGCAG TGGACTGTGT CCTCGGTGCA GAAACTACCA 420

GATTTGAGGG ACGAGGTCAA GGAGATATGA TAGGCCCGGA AGTTGCTGTG CCCCATCAGC 480

AGCTTGACGC GTGGTCACAG GACGATTTTC ACTGACACTG CGAACTCTCA GGACTACCGT 540

TACCAAGAGG TTAGGTGAAG TGGTTTAAAC CAAACGGAAC TCTTCATCTT AAACTACACG 600

TTGAAAATCA ACCCAATAAT TCTGTATTAA CTGAATTCTG AACTTTTCAG GAGGTACTGT 660

GAGGAAGAGC AGGCACCACC AGCAGAATGG GGAATGGAGA GGTGGGCAGG GGTTCCAGCT 720

TCCCTTTGAT TTTTTG 736

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1117 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

GGATCCGCCC GCCTTGGCCT CCCAAAGTGC TGGGATTACA GGCATGAGCC ACCGCTCCTG 60

GCTGAGTCTG CGATTTCTTG CCAGCTCTAC CCAGTTGTGT CATCTTAAGC AAGTCACTGA 120

ACTTCTCTGG ATTCCCTTCT CCTNNWGTAA AATAAGNATG TTATCTGNCC NNCCTGCCTT 180

GGGCATTGTG ATAAGGATAA GATGACATTA TAGAATNTNG CAAAATTAAA AGCGCTAGAC 240

AAATGATTTT ATGAAAATAT AAAGATTAGN TTGAGTTTGG GCCAGCATAG AAAAAGGAAT 300

GTTGAGAACA TTCCNTTAAG GATTACTCAA GCYCCCCTTT TGSTGKNWAA TCAGANNGTC 360

ATNNAMNTAT CNTNTGTGGG YTGAAAATGT TTGGTTGTCT CAGGCGGTTC CTACTTATTG 420

CTAAAGAGTC CTACCTTGAG CTTATAGTAA ATTTGTCAGT TAGTTGAAAG TCGTGACAAA 480

TTAATACATT CCTGGTTTAC AAATTGGTCT TATAAGTATT TGATTGGTNT AAATGNATTT 540

ACTAGGATTT AACTAACAAT GGATGACCTG GTGAAATCCT ATTTCAGACC TAATCTGGGA 600

GCCTGCAAGT GACAACAGCC TTTGCGGTCC TTAGACAGCT TGGCCTGGAG GAGAACACAT 660

GAAAGAMMGG TTTGWNTCTG NTTAWTGTAA TCTATGRAAG TGTTTTTWAT MACAGTATAA 720

TTGTMTGMAC AAAGTTCTGT TTTTCTTTCC CTTTNCAGAA CCTCAAGAGG CTTTGTTTTC 780

TGTGAAACAG TATTTCTATA CAGNTGCTCC AATGACAGAG TNACCTGCAC CGTTGTCCTA 840

CTTCCAGAAT GCACAGATGT CTGAGGACAA CCACCTGAGC AATACTGTAC GTAGCCAGGT 900

ACAGCGTCAG TYTCTNAAAC TGCCTYYGNC AGACTGGATT CACTTATCAT CTCCCCTCAC 960

CTCTGAGAAA TGCTGAGGGG GSTAGGNAGG GCTTTCTCTA CTTNACCACA TTTNATAATT 1020

ATTTTTGGGT GACCTTCAGC TGATCGCTGG GAGGGACACA GGGCTTNTTT AACACATAGG 1080

GTGTTGGATA CAGNCCCTCC CTAATTCACA TTTCANC 1117

(2) INFORMATION FOR SEQ ID NO:157:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 540 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

CTGCAGCTTT CCTTTAAACT AGGAAGACTT GTTCCTATAC CCCAGTAACG ATACACTGTA 60

CACTAAGCAA ATAGCAGTCA AACCCAAATG AAATTTNTAC AGATGTTCTG TGTCATTTTA 120

TNTTGTTTAT GTTGTCTCCC CCACCCCCAC CAGTTCACCT GCCATTTATT TCATATTCAT 180

TCAACGTCTN NNTGTGTAAA AAGAGACAAA AAACATTAAA CTTTTTTCCT TCGTTAATTC 240

CTCCCTACCA CCCATTTACA AGTTTAGCCC ATACATTTTA TTAGATGTCT TTTATGTTTT 300

TCTTTTNCTA GATTTAGTGG CTGTTTNGTG TCCGAAAGGT CCACTTCGTA TGCTGGTTGA 360

AACAGCTCAG GAGAGAAATG AAACGCTTTT TCCAGCTCTC ATTTACTCCT GTAAGTATTT 420

GGAGAATGAT ATTGAATTAG TAATCAGNGT AGAATTTATC GGGAACTTGA AGANATGTNA 480

CTATGGCAAT TTCANGGNAC TTGTCTCATC TTAAATGANA GNATCCCTGG ACTCCTGNAG 540

(2) INFORMATION FOR SEQ ID NO:158:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 509 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

CCCCGTCNAT GCATACTTTG TGTGTCCAGT GCTTACCTGG AATCCNGTCT TTCCCAACAG 60

CAACAATGGT GTGGTTGGTG AATATGGCAG AAGGAGACCC GGAAGCTCAA AGGAGAGTAT 120

CCAAAAATTC CAAGTATAAT GCAGAAAGTA GGTAACTYYY NTTAGATAMN ATCTTGATTT 180

TNCAGGGTCA CTGTTATAAG CTAACAGTAT AGNAATGTTT TTATCGTCTT TCTNKGGNCA 240

TAGACTCCTN KGAGAATCTC TTGAGAACTA TGATAATGCC CAGTAAATAC NCAGATAAGT 300

ATTTAAGGAG TNCAGATACT CAAANCCCAA CAATACNGTC AAAGCATCCT AGGTTAAGAC 360

AMCNCCCATT AAATACAGAA TACCAGCATG GAAAGGTTCA GGCTGAGGTT ATGATTGGGT 420

TTGGGTTTTG GGNNNGTTTT TTATAAGTCA TGATTTTAAA AAGAAAAAAT AAACTCTCTC 480

CAAACATGTA AAAGTAAGAA TCTCCTAAA 509

(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 823 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

CAGGAGTGGA CTAGGTAAAT GNAAGNTGTT TTAAAGAGAG ATGNGGNCNG GGACATAGTG 60

GTACACANCT GTAATGCTCA NCACTKATGG GGAGTACTGA AGGNGGNSGG ATCACTTGNG 120

GGTCNGGAAT NTGAGANCAG CCTGGGCAAN ATGGCGAAAC CCTGTCTCTA CTAAAAATAG 180

CCANAAWNWA GCCTAGCGTG GTGGCGCRCA CGCGTGGTTC CACCTACTCA GGAGGCNTAA 240

GCACGAGNAN TNCTTGAACC CAGGAGGCAG AGGNTGTGGT GARCTGAGAT CGTGCCACTG 300

CACTCCAGTC TGGGCGACMA AGTGAGACCC TGTCTCCNNN AAGAAAAAAA AAATCTGTAC 360

TTTTTAAGGG TTGTGGGACC TGTTAATTAT ATTGAAATGC TTCTYTTCTA GGTCATCCAT 420

GCCTGGCTTA TTATATCATC TCTATTGTTG CTGCTCTTTT TTACATTCAT TTACTTGGGG 480

TAAGTTGTGA AATTTGGGGT CTGTCTTTCA GAATTAACTA CCTNNGTGCT GTGTAGCTAT 540

CATTTAAAGC CATGTACTTT GNTGATGAAT TACTCTGAAG TTTTAATTGT NTCCACATAT 600

AGGTCATACT TGGTATATAA AAGACTAGNC AGTATTACTA ATTGAGACAT TCTTCTGTNG 660

CTCCTNGCTT ATAATAAGTA GAACTGAAAG NAACTTAAGA CTACAGTTAA TTCTAAGCCT 720

TTGGGGAAGG ATTATATAGC CTTCTAGTAG GAAGTCTTGT GCNATCAGAA TGTTTNTAAA 780

GAAAGGGTNT CAAGGAATNG TATAAANACC AAAAATAATT GAT 823

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 945 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

GTTNTCCNAA CCAACTTAGG AGNTTGGACC TGGGRAAGAC CNACNTGATC TCCGGGAGGN 60

AAAGACTNCA GTTGAGCCGT GATTGCACCC ACTTTACTCC AAGCCTGGGC AACCAAAATG 120

AGACACTGGC TCCAAACACA AAAACAAAAA CAAAAAAAGA GTAAATTAAT TTANAGGGAA 180

GNATTAAATA AATAATAGCA CAGTTGATAT AGGTTATGGT AAAATTATAA AGGTGGGANA 240

TTAATATCTA ATGTTTGGGA GCCATCACAT TATTCTAAAT AATGTTTTGG TGGAAATTAT 300

TGTACATCTT TTAAAATCTG TGTAATTTTT TTTCAGGGAA GTGTTTAAAA CCTATAACGT 360

TGCTGTGGAC TACATTACTG TTNCACTCCT GATCTGGAAT TTTGGTGTGG TGGGAATGAT 420

TTCCATTCAC TGGAAAGGTC CACTTCGACT CCAGCAGGCA TATCTCATTA TGATTAGTGC 480

CCTCATGNCC CTGKTGTTTA TCAAGTACCT CCCTGAATGG ACTGNGTGGC TCATCTTGGC 540

TGTGATTTCA GTATATGGTA AAACCCAAGA CTGATAATTT GTTTGTCACA GGAATGCCCC 600

ACTGGAGTGT TTTCTTTCCT CATCTCTTTA TCTTGATTTA GAGAAAATGG TAACGTGTAC 660

ATCCCATAAC TCTTCAGTAA ATCATTAATT AGCTATAGTA ACTTTTTCAT TTGAAGATTT 720

CGGCTGGGCA TGGTAGCTCA TGCCTGTAAT CTTAGCACTT TGGGAGGCTG AGGCGGGCAG 780

ATCACCTAAG CCCAGAGTTC AAGACCAGCC TGGGCAACAT GGCAAAACCT CGTATCTACA 840

GAAAATACAA AAATTAGCCG GGCATGGTGG TGCACACCTG TAGTTCCAGC TACTTAGGAG 900

GCTGAGGTGG GAGGATCGAT TGATCCCAGG AGGTCAAGNC TGCAG 945

(2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

Tyr Thr Pro Phe
1

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

Ser Thr Pro Glu
1

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

CATTCACTGA GGACACACC 19

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

TGTAGAGCAC CACCAAGA 18

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

GCATGGTGTG CATCCACT 18

(2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

GGACCACTCT GGGAGGTA 18

(2) INFORMATION FOR SEQ ID NO:167:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

AAACTTGGAT TGGGAGAT 18

(2) INFORMATION FOR SEQ ID NO:168:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

Asn Asp Asn Arg Glu Arg Gln Glu His Asn Asp Arg Arg Ser Leu
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:169:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

Lys Asp Gly Gln Leu Ile Tyr Thr Pro Phe Thr Glu Asp Thr Glu
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:170:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

Glu Ala Gln Arg Arg Val Ser Lys Asn Ser Lys Tyr Asn Ala Glu

1 5 10 15

(2) INFORMATION FOR SEQ ID NO:171:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

Ser His Leu Gly Pro His Arg Ser Thr Pro Glu Ser Arg Ala Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:172:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

CAGAGGATGG AGAGAATAC 19

(2) INFORMATION FOR SEQ ID NO:173:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

GGCTCCCCAA AACTGTCAT 19

(2) INFORMATION FOR SEQ ID NO:174:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

GCCCTAGTGT TCATCAAGTA 20

(2) INFORMATION FOR SEQ ID NO:175:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

AAAGCGGGAG CCAAAGTC 18

(2) INFORMATION FOR SEQ ID NO:176:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

TCACAGAAGA TACCGAGACT 20

(2) INFORMATION FOR SEQ ID NO:177:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

CCCAACCATA AGAAGAACAG 20

(2) INFORMATION FOR SEQ ID NO:178:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

TCTGTACTTT TTAAGGGTTG TG 22

(2) INFORMATION FOR SEQ ID NO:179:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

ACTTCAGAGT AATTCATCAN CA 22

(2) INFORMATION FOR SEQ ID NO:180:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

GACTCCAGCA GGCATATCT 19

(2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

GATGAGACAA GTNCCNTGAA 20

(2) INFORMATION FOR SEQ ID NO:182:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

TTAGTGGCTG TTTNGTGTCC 20

(2) INFORMATION FOR SEQ ID NO:183:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

CACCCATTTA CAAGTTTAGC 20

C' cont